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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 144 Seconds
(without alignments)
6405.058 Million cell updates/sec

Title: US-10-725-841-1
Perfect score: 1662
Sequence: 1 atgggctccagatctttac.....gagccactacgaaatgtga 1662

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1452.4	87.4	1662	3	US-09-232-479-10
2	1452.4	87.4	1662	4	US-09-784-990-10
3	1452.4	87.4	2176	1	US-07-778-890A-2
4	1431.6	86.1	3825	6	5310678-2
5	1412.4	85.0	1662	2	US-08-663-566A-12
6	1412.4	85.0	1662	2	US-08-023-610-12
7	1412.4	85.0	1662	2	US-08-288-065A-12
8	1412.4	85.0	1662	2	US-08-362-240A-12
9	1412.4	85.0	1662	3	US-08-804-372A-10
10	1412.4	85.0	1662	5	PCT-US95-10245-12
11	1412.4	85.0	4177	2	US-08-484-575A-12
12	1412.4	85.0	4177	3	US-08-477-459-12
13	1412.4	85.0	4177	3	US-08-479-869-12
14	1412.4	85.0	4177	3	US-08-486-414-12
15	1412.4	85.0	4177	5	PCT-US94-01826A-12
16	1412.4	85.0	4177	5	PCT-US94-02252A-12
17	137.6	8.3	1685	1	US-08-105-483-370
18	137.6	8.3	1685	1	US-08-709-209-370
19	137.6	8.3	1685	1	US-08-458-101-370
20	117	7.0	1656	2	US-08-700-548-3
21	100.4	6.0	2136	1	US-08-321-587-1
22	92.8	5.6	2113	1	US-08-224-657-87
23	92.8	5.6	2113	4	US-09-354-138-87
24	92.8	5.6	4343	1	US-08-224-657-93
25	92.8	5.6	4343	4	US-09-354-138-93
26	92.8	5.6	4604	1	US-08-224-657-96
27	92.8	5.6	4604	4	US-09-354-138-96

28	92.8	5.6	4965	3	US-08-675-566-22	Sequence 22, Appl
29	92.8	5.6	5147	3	US-08-675-566-24	Sequence 24, Appl
30	92.8	5.6	5241	3	US-08-675-566-23	Sequence 23, Appl
31	92.8	5.6	8792	3	US-08-675-566-25	Sequence 25, Appl
32	88	5.3	2521	1	US-08-368-803-16	Sequence 16, Appl
33	88	5.3	2521	2	US-08-578-096A-18	Sequence 18, Appl
34	88	5.3	2521	3	US-08-790-517-8	Sequence 8, Appl
35	88	5.3	2521	3	US-09-240-426-18	Sequence 18, Appl
36	88	5.3	2521	3	US-09-219-932-14	Sequence 14, Appl
37	88	5.3	2521	4	US-09-362-831-8	Sequence 8, Appl
38	84.2	5.1	15894	1	US-08-348-891A-1	Sequence 1, Appl
39	84.2	5.1	15894	1	US-08-905-817-1	Sequence 1, Appl
40	82.6	5.0	1653	3	US-09-230-944-17	Sequence 17, Appl
41	82.6	5.0	1653	4	US-09-873-233A-17	Sequence 17, Appl
42	82.6	5.0	1687	1	US-08-279-700-15	Sequence 15, Appl
43	82.2	4.9	15462	3	US-09-073-492-1	Sequence 1, Appl
44	81	4.9	1653	3	US-09-230-944-19	Sequence 19, Appl
45	81	4.9	1653	4	US-09-873-233A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-232-479-10
; Sequence 10, Application US/09232479
; Patent No. 6221362
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/232,479
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: 96/09339
; EARLIER FILING DATE: 1996-07-19
; EARLIER APPLICATION NUMBER: PCT/FR97/01326
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-232-479-10

Query Match	87.4%	Score	1452.4	DB	3	Length	1662
Best Local Similarity	92.1%	Pred. No.	0				
Mismatches	1531	Conservative	0	Mismatches	131	Indels	0
Gaps	0						
Qy	1	ATGGGCTCCAGATCTTCTTACCAGATCCAGTACCTCTGATGCTGACCGTCCGGTCCGG	60				
Db	1	ATGGGCTCCAGATCTTCTTACCAGATCCGGTACCTCTAATGCTGATCATCCGAAACCGG	60				
Qy	61	CTGGCACTGATGTCGTCGCGAAGCTCCCTTGTGATGCGAGGCTCTTTGACGTGCA	120				
Db	61	CTGACACTGATGTCGTCGTCGCGAAGCTCTTTGATGCGAGGCTCTTTGCGGTGCA	120				
Qy	121	GGGATGTCGTCGAGGAGCAAAAGCAGTCACATATACACCTCATCTCAGACAGGTGCA	180				
Db	121	GGGATGTCGTCGAGGAGCAAAAGCAGTCACATATACACCTCATCTCAGACAGGTGCA	180				
Qy	181	ATCATAGTCAAGTACTTCCCAATATGCCCCAAGATTAAGAGCGGTGTGCAAAAGCCCCG	240				
Db	181	ATCATAGTCAAGTACTTCCCAATATGCCCCAAGATTAAGAGCGGTGTGCAAAAGCCCCA	240				
Qy	241	TTGGAGCGTACACAGGACATTGACTTCTTGTACACCCCTTGTGATTTCTATTCTGT	300				
Db	241	TTGGAGCGTACACAGGACATTGACTTCTTGTACACCCCTTGTGATTTCTATTCTGT	300				
Qy	301	AGGATACAAGTCTGTGACTTACATCTGGAGGAGGAAACAGGACCCCTTATAGGCGCC	360				

Db 301 AGGATACAAAGAGTCTGTGACTCTCCGGAGGAAGGAGACAGAGCGCTTTATAGTGGC 360
QY 361 ATTATCGGCGGTGACGCTCTCGGGGTTCGAAACCGCTGCACAGATACACAGAGCTTCGGCT 420
Db 361 ATTATCGGCGGTGAGCTCTCGGGGTTCGAAACCGCTGCACAGATACACAGAGCTTCGGCT 420
QY 421 CTGATACAAAGCAACCAAAATGTCGCAACATCTCCGGCTTAAAGAGAGAAATGCTGCA 480
Db 421 CTGATACAAAGCAACCAAGATGTCGCAACATCTCCGGCTTAAAGAGAGAAATGCTGCA 480
QY 481 ACCAATGAGGCTGTGCACAGGTCACTGATGATATCAAACTAGCAGTGGCAGTGG 540
Db 481 ACCAATGAGGCTGTGCACAGGTCACTGATGATATCAAACTAGCAGTGGCAGTGG 540
QY 541 AAGATGCAACAATTTGTTAATGACCAAGTTTAAATAAAGAGCTCAGGAATGCACTGTATA 600
Db 541 AAGATGCAACAATTTGTTAATGACCAAGTTTAAATAAAGAGCTCAGGAATGCACTGTATA 600
QY 601 AAAATTAACCAAGAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 660
Db 601 AAAATTAACCAAGAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATGACTACAGTA 660
QY 661 TTGCGGCAACAATCACTCCCTGCTTAAACCAAGCTGATCAATCAAGCGCTTTACAA 720
Db 661 TTGCGGCAACAATCACTCCCTGCTTAAACCAAGCTGATCAATCAAGCGCTTTACAA 720
QY 721 CTAGCTGTGGGAATATGATTAATGATTTGTTGATTAAGTTAGGTAGGTAAGCAACCACT 780
Db 721 CTAGCTGTGGGAATATGATTAATGATTTGTTGATTAAGTTAGGTAGGTAAGCAACCACT 780
QY 781 AGCTCAATTAATGTTAGCGGCTGTATCCCGCAACCTATTTCTGACGACTCAGACT 840
Db 781 AGCTCAATTAATGTTAGCGGCTGTATCCCGCAACCTATTTCTGACGACTCAGACT 840
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Db 841 CAGCTCTTGGGTATACAGTAACCTACCTCAGTCGGGAACCTGAATAATATGCGTCC 900
QY 901 ACCTACTTTGGAACCTCTGTAGTAACTAACCAAGGATTTGCTCAGCACTCGTCCA 960
Db 901 ACCTACTTTGGAACCTCTGTAGTAACTAACCAAGGATTTGCTCAGCACTCGTCCA 960
QY 961 AAGTGTGTGATGAGGTCGGTTCGGTGTATGATAGAACTTGACCTCATCTGTATAGAG 1020
Db 961 AAGTGTGTGATGAGGTCGGTTCGGTGTATGATAGAACTTGACCTCATCTGTATAGAG 1020
QY 1021 ACCGATTTGGATCTATATGTTGATCAAGATAGTGAATCCCTATGTCCTGGTATTTAT 1080
Db 1021 ACCGATTTGGATCTATATGTTGATCAAGATAGTGAATCCCTATGTCCTGGTATTTAT 1080
QY 1081 TCCTGTTTGAACGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGGCGCACTCACT 1140
Db 1081 TCCTGTTTGAACGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGGCGCACTCACT 1140
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Db 1141 ACGCGGTACATGACTCTCAAGGCTCAGTTATTCGCAACTGTAAAGATGACAAATGTAGA 1200
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Db 1201 TGTGCAGACCCCGGCTATCATATCGCAAAATTTATGAGAGAGTGTCTCTTAATAGAT 1260
QY 1261 AGGCAATCATGCAATGCTTATCTTACGCGGATAACTTTGAGGCTCAGTGGGAATTT 1320
Db 1261 AGGCAATCATGCAATGCTTATCTTACGCGGATAACTTTGAGGCTCAGTGGGAATTT 1320
QY 1321 GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCGTGAAGGCAAT 1380
Db 1321 GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCGTGAAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACCACTCGGATAAGTATGCTTTAGATAAG 1440
Db 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACCACTCGGATAAGTATGCTTTAGATAAG 1440

RESULT 2

US-09-784-990-10

; Sequence 10, Application US/09784990

; Patent No. 6464984

; GENERAL INFORMATION:

; APPLICANT: AUDONNET, JEAN-CHRISTOPHE

; APPLICANT: BOUCHARDON, ANNABELLE

; APPLICANT: RIVIERE, MICHEL

; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA

; FILE REFERENCE: 454313-2260

; CURRENT APPLICATION NUMBER: US/09/784,990

; CURRENT FILING DATE: 2001-02-15

; PRIOR APPLICATION NUMBER: 96/09339

; PRIOR FILING DATE: 1996-07-19

; PRIOR APPLICATION NUMBER: PCT/FR97/01326

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 1662

; TYPE: DNA

; ORGANISM: Newcastle disease virus

US-09-784-990-10

Query Match

Best Local Similarity 87.4%; Score 1452.4; DB 4; Length 1662;

Matches 1531; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTCCCTTGTGATGCTGACCGTCCGGTCCG 60
Db 1 ATGGGCTCCAGATCTTCTACAGGATCCCGTACCTCTAATGCTGATCATCCGAACCGG 60
QY 61 CTGGCACTGAGTGGCTGTCTGTGCAAGCTCCCTTGTGATGGAGGCTCTTTGCAAGTCA 120
Db 61 CTGACACTGAGTGTATCCGCTGTGCAAGCTCTTGTGATGGAGGCTCTTTGCGGCTGA 120
QY 121 GGGATCTGTGTGACAGAGCAAGAGCTCAACATATACACCTCATCTCAGAGGCTCA 180
Db 121 GGGATCTGTGTAAAGAGATAAAGAGCTCAACATATACACCTCATCTCAGAGAGGCTCA 180
QY 181 ATCATAGTCAAGTTACTTCCCAAAATATGCCCAAGATAAGAGGCTGTGCAAAAGCCCG 240
Db 181 ATCATAGTTAAGTTACTTCCCGAATATGCCCAAGATAAGAGGCTGTGCAAAAGCCCA 240
QY 241 TTGAGGCGGTACAAAGGACATTTGACTATCTTTGCTCACTTTGCTGATTTCTATTCGT 300
Db 241 TTGAGGCGGTACAAAGGACATTTGACTATCTTTGCTCACTTTGCTGATTTCTATTCGT 300
QY 301 AGGATACAGAGTCTGTGACTACTTCTGGAGGAGGAAACAGGAGCGCTTTAGGGCC 360
Db 301 AGGATACAGAGTCTGTGACTACTTCTGGAGGAGGAGAGAGAGAGCTTTATAGGTGCC 360
QY 361 ATTATCGGCGGTGCACTCTCGGGGTTCGAAACCGCTGCACAGATAACAGAGCTTCGGCT 420
Db 361 ATTATCGGCGGTGCACTCTCGGGGTTCGAAACCGCTGCACAGATAACAGAGCTTCGGCT 420

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QY 421 CTGATACAGCCAAACCAAAATGCTGCCAATCCTCCGGCTTAAAGAGAGAAATGCTGCA 480
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Db 481 ACCAATGAGGCTGTGCACGAGGTCACCTGATGGAATATCAAACTAGCAGTGGCAGTAGGG 540
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Db 541 AAGATCGACGAATTTGTTCAATGACCAAGTTTCAATAATACAGCGCAAGAAATTTGGACTGTATA 600
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QY 781 AGCTCAATTAATGGTAGCGGCTGATCACCGGCAACCCCTATTCTGTACGACTCACAGACT 840
Db 781 AGCTCAATTAATGGTAGCGGCTTATCACCGGCAACCCCTATTCTGTACGACTCACAGACT 840
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Db 841 CAGATCTTGGGTATACAGGTAACCTTGGCTTCACTTGGGAACCTGAATAATATGCGTGCC 900
QY 901 ACCTACTTGGAAACCTTGTCTGTAAGTACAAACAAAGAAATTTGCCTCAGCACTCGTCCCA 960
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Db 1021 ACCGATTTGGATTTACTGTACAAGAAATAGTGACATTCCTATGCTCTCTCGTGGTATTAT 1080
QY 1081 TCCTGTTGAGCGGCAATACATCGGCTTGCACTGCTGCAAGACTGAAAGCGGCACTCACT 1140
Db 1081 TCCTGTTGAGCGGTAATACATCGGCTTGCACTGCTTCAAAGACTGAAAGCGGCACTTACT 1140
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Db 1201 TGTGCAGATCCCCAGGTATCATATCGCAAAATATGGAAGAGCTGTGTCTCTTAAATAGAT 1260
QY 1261 AGGCAATCATGCAATGCTTATCCTTAGACGGAAATACTTTGAGGCTCAGTGGGGAATTT 1320
Db 1261 AGGCACCTCATGCAAGCTTATCCTTAGACGGGATACTCTGAGGCTCAGTGGGGAATTT 1320
QY 1321 GATGCACTTATCAAGAATATCTCAATACAAGATTTCAAGTAACTGACAGGCAAT 1380
Db 1321 GATGCAACCTATCAAGAATAATCTCTATCAAGATTTCAAGTAACTGACAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTGGGAATGTCACAACTCGAATAAGTAACTGCTTTAGATAAG 1440
Db 1381 CTTGATATATCAACTGAGCTTGGGAATGTCACAACTCAATAAGTAACTGCTTAAATAG 1440
QY 1441 TTAGAGGAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACCTGACAGCACATCCGCT 1500
Db 1441 TTAGAGGAAGCAACAGCAAACTAGACAAGTCAATGTCAAACCTGACAGCACATCTGCT 1500
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Db 1501 CTCATTACCTACATCGTTTAACTGTCATATCTCTTGTTGGTACTTAGCCTGGTT 1560
QY 1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAGAAAGACCTTGTATGCTTGGG 1620
Db 1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAAAGACCTTGTATGCTTGGG 1620
QY 1621 AATAATACCTGTGATCAGATGAGAGCCACTACGAAAATGTGA 1662
Db 1621 AATAATACCTTGTATCAGATGAGAGCCACTACAAAATATGA 1662
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RESULT 3

US-07-778-890A-2

; Sequence 2, Application US/07778890A

; Patent No. 5266489

; GENERAL INFORMATION:

; APPLICANT: 1.REV-SENELONGE Arielle

; APPLICANT: 2.KOHN Gilla

; TITLE OF INVENTION: recombinant herpes viruses,in particular for the

; TITLE OF INVENTION: production of vaccines,process for preparing them,plasmids pro

; TITLE OF INVENTION: during this process and vaccines obtained.

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Larson and Taylor

; STREET: 727 Twenty-Third Street,South

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette-5.25 inch,360Kb storage

; COMPUTER: IBM PC/XT/AT or compatibles

; OPERATING SYSTEM: PC-DOS or MS-DOS version 2.2 or above

; SOFTWARE: KEDIT or any ASCII Text Editor

; CURRENT APPLICATION DATA: 07/778,890

; APPLICATION NUMBER: US/07/778,890A

; FILING DATE: 19920103

; CLASSIFICATION: 435

; PRIORITY INFORMATION:

; APPLICATION NUMBER: FR9003105,PCT/FR/91/00184

; FILING DATE: 12-MAR-1990,07-MAR-1991

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2176 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: cDNA to genomic RNA

; HYPOTHETICAL: yes

; ANTI-SENSE: no

; ORIGINAL SOURCE:

; ORGANISM: Newcastle disease virus (NDV)

; STRAIN: Texas strain

; INDIVIDUAL ISOLATE: chicken

; IMMEDIATE SOURCE:

; LIBRARY: plasmid

; CLONE: pNDV 108

; FEATURE:

; NAME/KEY: part of matrix protein gene and fusion protein gene

; LOCATION: from to description

; LOCATION: 1 271 matrix protein gene

; LOCATION: 431 2092 fusion protein gene

US-07-778-890A-2

Query Match

Best Local Similarity 87.4%; Score 1452.4; DB 1; Length 2176;

Matches 1531; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGCTGACCGGTCGCG 60

Db 431 ATGGGCTCCAGATCTTCTACAGGATCCCGGTACCTCTAATGCTGATCATCCGAACCGG 490

O 61 CTGGCACTGAGTTGGTCTGTGCGCAAGCTCCCTTGATGGCAGGCTCTTGCAGTGA 120
121 GGGATTGGTGCACAGGAGCAAAAGCAGTCAACATATACACCTCTCTCAGACAGGCTCA 180
551 GGGATCGTGTAAACAGGAGATAAAGCAGTCAACATATACACCTCTCTCAGACAGGCTCA 610
181 ATCATAGTCAAGTTACTCCCAATATGCCCCAAGATAAAGAGCGGTGTCAAAAGCCCCG 240
611 ATCATAGTTAAGTTACTCCCGAATATGCCAAGGCAAAAGAGGTGTGTGCAAAAGCCCCA 670
241 TTGGAGGCGTCAACAGGACATTTGACTACTTTGCTCACCCTTGGTGGATTTCTATCGT 300
671 TTGGAGGCGTCAACAGGACATTTGACTACTTTGCTCACCCTTGGTGGATTTCTATCGC 730
301 AGGATACAAGAGTGTGTGACTCATCTGGAGGAGGAAACAGGAGCGCTTATAGCGGCC 360
731 AGGATACAAGAGTGTGTGACTCATCTCCGAGGAGGAGACAGAGCGCTTATAGGTGCC 790
361 ATTATCGGCGTGCAGCTCTCGGGTTCGAAACCGCTGACAGATTAACAGCAGCTTCGGCT 420
791 ATTATCGGCGTGTAGCTCTTGGGTTGCGAGCTGCAACAGATTAACAGCAGCTTCGGCC 850
421 CTGATACAAGCCAAACCAAAATGCTGCCAATCTCCCGCTTAAAGAGAGAAATTCGTGCA 480
851 CTGATACAAGCCAAACCAAGATGCTGCCAATCTCCCGCTTAAAGAGAGCAATTCGTGCA 910
481 ACCAATGAGGTGTGCAAGAGTCTAGTGAATATCAAACTAGCAGTGGCAGTTGGG 540
911 ACCAATGAGGTGTGCAAGAGTCTAGTGAATATCAAACTAGCAGTGGCAGTTGGG 970
541 AGAGTGCAGCAATTTGTTAATCAGCAGTTAATAAAGCTCAGGAATGAGCTGTATA 600
971 AAGATGCAACAGTTTGTCAATACCAAGTTCAATATACAGCGCAAGAAATTTGACTGTATA 1030
601 AAAATTAACAGCAGGTGGTGTAGAACTCAACCTGTATCTAACTGAATTTGACTACAGTA 660
1031 AAAATTAACAGCAGGTGGTGTAGAACTCAACCTGTATCTAACTGAATTTGACTACAGTA 1090
661 TTGGGCGCAAAATCACTTCCCTGCTTAAACAGCTGACTATCCAGCGCTTTTACAAT 720
1091 TTGGGCGCAAAATCACTTCCCTGCTTAAACAGCTGACTATCCAGCGCTTTTACAAT 1150
721 CTAGCTGTGGGAATATGATTAATCTGTTGCTAAGTTAGGTAGGTAAGGTAAGGTAAGG 780
1151 CTAGCTGTGGGAATATGATTAATCTGTTGCTAAGTTAGGTAGGTAAGGTAAGGTAAGG 1210
781 AGCTCAATTAATTTGGTGGGCTGTATCAGCGCAACCTTATCTCTAGCAGCTCAGAGCT 840
1211 AGCTCAATTAATTTGGTGGGCTGTATCAGCGCAACCTTATCTCTAGCAGCTCAGAGCT 1270
841 CAGCTCTTGGGTATACAGGTAACCTTACCTCAGTGGGAACTGAATTAATGCGTGC 900
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901 ACCTACTTTGGAAACCTTGTCTGTAAGTACAACCAAGGATTTGCTCAGCACTCGTCCCA 960
1331 ACCTACTTTGGAAACCTTGTCTGTAAGTACAACCAAGGATTTGCTCAGCACTCGTCCCA 1390
961 AAGGTGGTGAAGAGTGGTTCGGTGTAGAGAACTTGACACCTCTATCTGTATAGAG 1020
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1021 ACCGATTTGGATCTATATTTGACAGAAATAGTGAATTCCTTATCTCTCTGGTATTTAT 1080
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1081 TCCTGTTTGGAGCGGCAATACATCGGCTTGCATGTACTCGAAGCTGGAAGGCGCACTCACT 1140
1511 TCCTGTTTGGAGCGGCAATACATCGGCTTGCATGTACTCGAAGCTGGAAGGCGCACTCACT 1570

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OY 1201 TGTGCAGACCCCGGGTATCATATCGAAAAATTATGGAGAAGCTGTCTCTTAAATAGAT 1260
Db 1631 TGTGCAGATCCCGGAGTATCATATCGAAAAATTATGGAGAAGCTGTCTCTTAAATAGAT 1690
OY 1261 AGGCAATCATGAATGTCTCTATCTTAGACGGAATACTTTGAGGCTCAGTGGGGAATTT 1320
Db 1691 AGGCACTCATGCAAGCTCTTATCTTAGACGGAATACTCTGAGGCTCAGTGGGGAATTT 1750
OY 1321 GATGCAACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTAACTCTGACAGCAAT 1380
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OY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACCACTCGATAAGTAAGTCTTAAATAG 1440
Db 1811 CTTGATATATCAACTGAGCTTGGGAATGTCAACCACTCAATAAGTAAATGSCCTGAATAG 1870
OY 1441 TTAGAGGAAGCAACAGCAACTAGACAAAGTCAATGTCAAACTGACCGAGCAATCCGCT 1500
Db 1871 TTAGAGGAAGCAACAGCAACTAGACAAAGTCAATGTCAAACTGACCGAGCAATCCGCT 1930
OY 1501 CTCATCACCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
Db 1931 CTCATCACCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1990
OY 1561 CTAGCATCTACCTGTATGATCAAGCAAAAGGCGCAACAGAGCACTTGTATGCTTGGG 1620
Db 1991 CTAGCATCTACCTGTATGATCAAGCAAAAGGCGCAACAGAGCACTTGTATGCTTGGG 2050
OY 1621 AATAATACCTGTGATCAGATGAGAGCCACTACGAAAAATGTGA 1662
Db 2051 AATAATACCTGTGATCAGATGAGAGCCACTACGAAAAATGTGA 2092

RESULT 4

5310678-2

; Patent No. 5310678

; APPLICANT: Bingham, Richard W.; Chambers, Philip; Emerson, Peter

; T.; Millar, Neil S.

; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES

; NUMBER OF SEQUENCES: 3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/438,945

; FILING DATE: 17-NOV-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 885,765

; FILING DATE: 15-JUL-1986

; SEQ ID NO.: 2

; LENGTH: 3825

5310678-2

Query Match

Best Local Similarity 86.1%; Score 1431.6; DB 6; Length 3825;

Matches 1518; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

OY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGTGCTGACCGTCCGGTCCGC 60
Db 47 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGTGCTGACCGTCCGGTCCGC 106
OY 61 CTGGCACTGAGTTGGTCTGTGCGCAAGCTCCCTTGAATGAGGCGCTCTTGCAGCTGCA 120
Db 107 CTGGTACGAGTTGGTCTGTGCGCAAGCTCCCTTGAATGAGGCGCTCTTGCAGCTGCA 166
OY 121 GGGATTGTGGTGAAGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 180
Db 167 GGAATTTGGTGAAGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGATCA 226
OY 181 ATCATAGTCAAGTTACTCCGAAATATGCCCAGAAAGTAAGAGGCGTGTGCAAAAGCCCG 240
Db 227 ATCATAGTCAAGTTACTCCGAAATATGCCCAGAAAGTAAGAGGCGTGTGCAAAAGCCCG 286

241 TTGGAGCGGTAAACAGGACATTTGACTATCTTGTCTACCCCTTGTGTGATCTATTCGT 300
Db |||||
287 TTGGATGCATACACAGGACATTTGACACATTTGCTACCCCTTGTGTGACTATCCGT 346
Qy |||||
301 AGGATACAGAGCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCTTATAGCGCC 360
Db |||||
347 AGGATACAGAGCTGTGACTACATCTGGAGGAGGAGAGAGAAACGCTTATAGCGCC 406
Qy |||||
361 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACCGCTGCAAGAGTAAACAGAGCTTCGGCT 420
Db |||||
407 ATTATCGGCGGTGAGCTCTCGGGGTTGCAACCGCTGCAAGAGTAAACAGAGCTTCGGCT 466
Qy |||||
421 CTGATACAGCCAAACCAAAATGCTGCGGTTGCAACCGCTTAAAGAGAGAAATGCTGCA 480
Db |||||
467 CTGATACAGCCAAACCAAAATGCTGCGGTTGCAACCGCTTAAAGAGAGCAATGCGCA 526
Qy |||||
481 ACCAATGAGGCTGTGACAGAGGTCACTGATGGATTATCAAACTAGCAGTGGCAGTTGGG 540
Db |||||
527 ACCAATGAGGCTGTGACAGAGGTCACTGATGGATTATCGCAACTAGCAGTGGCAGTTGGG 586
Qy |||||
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Db |||||
587 AAGATCAGCAGTTTGTAAATGACCAATTTAAATAAAACAGCTCAGGAATTTAGGCTGCATC 646
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767 CTAGCTGTGGGAATTTGATTAATGACTTACTTGTGACTAAGTTAGGTGAGGAAACCAACTC 826
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901 ACCTACTTGAACCTTGTCTGTAAGTAAACCAAGGATTTGCTCAGCACTGCTCCCA 960
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Qy |||||
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Db |||||
1187 ACGCATACATGACTCTCAAGGTGCTTATTCGCACTGTAAGATGACAACTGATAGA 1246
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1321 GATGCAACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTAACTGTGACAGGCAAT 1380
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1547 CTGATCACTATATCTTTTAACTGTCTATCTCTTGTGTTGTGTTATGCTTATGCTGCTGTT 1606
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1607 CTAGCATGCTACCTGTATGTATAGCAAAAGCGCAACAAAGACCTTATGTTATGCTTGGG 1666
Qy |||||
1621 AATAATACCTGTGATGATGAGAGCCACTTACGAAATGTGA 1662
Db |||||
1667 AATAATACCTGTGATGATGAGAGCCACTTACGAAATGTGA 1708

RESULT 5

US-08-663-566A-12
; Sequence 12, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,566A
; FILING DATE: June 13, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-663-566A-12

Query Match 85.0%; Score 1412.4; DB 2; Length 1662;

Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Db 1 ATGGGCTCCAGATCTTACAGGATCCAGTACCTCTGATCGTACCGCTCGGGTCGG 60
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Db 121 GGGATTTGGTGTACAGGAGACAAAGCAGTCAATATACCTCTCATCTCTCAGAGGTCA 180
QY 181 ATCATAGTCAAGTCTTCTCCCAATATGCCCAAGATTAAGAGCGGTGTGCAAAAGCCCG 240
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QY 241 TTGGAGGGGTACAACAGGACATTGACTCTTTGCTCACCCCTTTGGTGATTCTATTCTGT 300
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Db 1021 ACCGATTTGGATCTATATTGTACAAGATAGTACATCCCTATGCTCTCGGTATTAT 1080
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Db 1621 AATAATACCTGGATCAGATGAGAGCCACTAGCAAAATGTGA 1662
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RESULT 6

US-08-023-610-12
; Sequence 12, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; APPLICANT: Macdonald Ph.D., Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/023,610
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550

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; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; US-08-023-610-12

Query Match      85.0%; Score 1412.4; DB 2; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGAGCGTCCGGTCCGG 60
DB 1 ATGGGCTCCAGACTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTCCGG 60
QY 61 CTGGCACTGAGTTGCGTCTGTCCGACAAAGCTCCCTTGATGGCAGCGCTCTTGCAGTGC 120
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QY 121 GGAATTGTGGTACAGGAGACAAAGCAGTCAACATATACACCTCATCCGACAGGATCA 180
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US-08-288-065A-12
; Sequence 12, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662
US-08-288-065A-12

Query Match 85.0%; Score 1412.4; DB 2; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
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661 TTGGGCCCCAACAATCATTCCCTGCTTAACCCAGCTGACTATCCAGGCGCTTTACAAAT 720
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721 CTAGCTGGTGGGAATATGGAATTTACTTTGTAGCTAAGTTAGGTAGGGAACCAACCAATC 780
721 CTAGCTGGTGGGAATATGGAATTTACTTTGTAGCTAAGTTAGGTAGGGAACCAACCAATC 780
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901 ACCTACTTGGAAACCTTCTGTAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 960
961 AAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020
961 AAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020
1021 ACCGATTTGGATCTATTTGTACAGATAGTGCATTTCCCTATCTCTCTCTCTCTCTCTCT 1080
1021 ACTGACTTAGATTTATATTTGTACAGATAGTGCATTTCCCTATCTCTCTCTCTCTCTCT 1080
1081 TCCTGTTTGGGCGCAATACATCGGCTGTATGTAACAGAGCTGAAGAGGCGCACTCACT 1140
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1141 AGCGGTAATGACTCTCAAGGCTCAGTTATTTGCAATTTGCAATTTGCAATTTGCAATTTG 1200
1141 ACACATATATGACTATCAAGGCTCAGTCACTGCTAATTTGCAATTTGCAATTTGCAATTTG 1200
1201 TGTGAGAGCCCGGGTATCATATCGCAAAATTTGAGAGGCTGCTCTCTCTCTCTCTCTCT 1260
1201 TGTGAGAGCCCGGGTATCATATCGCAAAATTTGAGAGGCTGCTCTCTCTCTCTCTCTCT 1260
1261 AGGCAATCATGCAATGTCTCTTATAGAGGATTAACCTTTGAGGCTCAGTGGGGAATTT 1320
1261 AGGCAATCATGCAATGTCTCTTATAGAGGATTAACCTTTGAGGCTCAGTGGGGAATTT 1320
1321 GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCTGAGAGGCAAT 1380
1321 GATGCACTTATCAAAAGATATCTCAATACAGATTTCTCAAGTATCTGAGAGGCAAT 1380
1381 CTGATATCTGCACTGAGCTTTGGGAATGTCAACCACTGATGATGATGATGATGATGATGAT 1440
1381 CTGATATCTGCACTGAGCTTTGGGAATGTCAACCACTGATGATGATGATGATGATGATGAT 1440
1441 TTAGAGGAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCCGCT 1500
1441 TTAGAGGAACCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACAGCAATCCGCT 1500
1501 CTGATCACTATGCTTTTAACTGCTATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1560
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1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAGAGACCTTTGTTGTTGTTGTTG 1620
1561 CTAGCATGCTACCTGATGTACAAGCAAAAGGCGCAACAGAGACCTTTTATGTTGTTGTTG 1620
1621 AATAATACCTTGGATCAGATGAGAGCCACTAGAGAAATGTGA 1662

Db 1621 AATAATACCTAGATCAGATGAGAGCCACTACAAAAATGTGA 1662

RESULT 8

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US-08-362-240A-12
; Sequence 12, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
US-08-362-240A-12

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Query Match	85.0%	Score 1412.4	DB 2	Length 1662
Best Local Similarity	90.6%	Pred. No. 0		
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Qy	1	ATGGGCTCCAGATCTTCTACAGAGATCCCAGTACTCTGTATGCTGTCAGCGTCCGGGTGCGG	60	
Db	1	ATGGGCTCCAGACCTTCTACCAAGAACCCAGACCTATGATGCTGTGACTATCCGGGTGCGG	60	
Qy	61	CTGGCACTGAGTTGCGTCTGTGCCACAAAGTCCCTTGTATGGCAGGCCTTTGCAGCTGCA	120	
Db	61	CTGGTACTGAGTTGCACTGTCTCGGAAACTCCATTGATGGCAGGCCTCTTCGAGCTGCA	120	
Qy	121	GGGATTTGGTGCAGAGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA	180	
Db	121	GGAATTTGGTTACAGGAGCAAAAGCAGTCAACATATACACCTCATCCAGACAGGATCA	180	
Qy	181	ATCATAGTCAAGTTACTCCCAAAATATGCCAAAGATAAGAGGGGTGTGCAAAAGCCCGG	240	
Db	181	ATCATAGTTAAGTCTCTCCCGAATCTGCCAAAGATAGGAGGCATGTGCGAAGAGCCCCC	240	
Qy	241	TTGAGGCGGTCAACAGSACATTGACTATTGTCTCACCCCCCTTGGTGTATTCTATTGCT	300	

241	TTGGATGCTATACAACAGGACATTGACCACTTTTGGCTCACCCCTTTGGTGACTCTATCCGT	300
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301	AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGGAACACAGGAGCGGCGCTTATAGGGGCC	360
361	ATTATCGGCGGTGCAGCTCTCGGGGTTCGAACCGCTGCACAGATAACAGCAGCTTCCGCT	420
361	ATTATTGGGCGTGGCTCTTTGGGGTTGCAACTGGCGCACAAATAACAGCGGCGCGAGCT	420
421	CTGATACAAGCCAAACCAAAATGCTGCCAATCCTCCGGCTTAAAGAGAGAAATGCTGCA	480
421	CTGATACAAGCCAAACCAAAATGCTGCCAATCCTCGACTTAAAGAGAGCATTCGCGCA	480
481	ACCAATGAGGCTGTGCACGAGTCACTGATGGATTATCAAACTAGCAGTGGCAGTTGGG	540
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541	AGATGAGCAATTTGTTTAATGACCAAGTTTAATAAACAAGCTCAGGAATTGGAGCTGTATA	600
541	AGATGAGCAGTTTCGTTAATGACCAATTTAATAAACAAGCTCAGGAATTAGACTGCATC	600
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661	TTGGGCGCAAAATCACTTCCCCTGGCTTAACCCAGCTGACTACTCCAGGCGCTTTACAAT	720
661	TTGGGACCAAAATCACTTCACTCACTGCTTAAACAAGCTGACTATTCAGGCACITTTACAAT	720
721	CTAGCTTGGTGGGAATATGGAATTACTTTTGACTGAAGTTAGGTGAGGGAACAACCAATC	780
721	CTAGCTGGTGGGAATATGGAATTACTTTTACCTAAAGTTAGGTATAGGGAACAATCAATC	780
781	AGCTCATTAATTTGGTAGCGGCTGATCACCGGCAACCCCTATTCGTACGACTCACAGACT	840
781	AGCTCATTAATTCGGTAGCGGCTTAATCACCGGTAAACCCCTATTCGTACGACTCACAGACT	840
841	CAGCTCTTGGGTATACAGGTAACCCCTACCTCAGTCGGGAACCTGGAATAATATCGTGCC	900
841	CAACTCTTGGGTATACAGGTAACTCTACCTTCAGTCGGGAACCTAATAATATCGGTGCC	900
901	ACCTACTTGGAAACCTTGTCTGTAAGTAPACAACCAAGGAATTCGCTCAGCACTCGTCCCA	960
901	ACCTACTTGGAAACCTTATCCGTAAAGCACCAACACAGGGGAATTCGCTCGGCACITGTCCCA	960
961	AAGTGGTGATGAAGTTCGGTCCGTGATAGAGAAGCTTGACACCTCATACTGTPATAGG	1020
961	AAGTGGTGACACGGGTCCGTTCTGTGATAGAGAAGCTTGACACCTCATACTGTPATAGAA	1020
1021	ACCGATTGGATCTATATTGTACAAGAATATGATGACATTCCTCATGTCTCTGGTATTAT	1080
1021	ACTGACTTAGATTATATTGTACAAGNAATGATAAGTTTCCTATGTCCCTGGTATTAT	1080
1081	TCCTGTTGAGCGGCAATACATCGGCTGTATGTACTCAAAGACCGAAGCGCACTTACT	1140
1081	TCCTGTTGAGCGGCAATACATCGGCTGTGATGTACTCAAAGACCGAAGCGCACTTACT	1140
1141	ACGCGGTACATGACTCTCAAGGCTCAGTTATTGGCCAAGCTGTAGATGACAACATGTAGA	1200
1141	ACACCATATATGACTATCAAGGCTCAGTCATCGCTAACTTGAAGATGACAACATGTAGA	1200
1201	TGTGCAAGCCCCCGGTATCATATCGAAAAATTTATGGGAAGCTGTGTCTCTAATAGAT	1260
1201	TGTGTAAACCCCCCGGTATCATATCGAAAAATTTATGGGAAGCGCGTGTCTCTAATAGAT	1260
1261	AGGCAATCATGCAATGTCTTATCCTTAGACGGAATAACTTTTGAGGCTCAGTGGGGAATTT	1320
1261	AAACAATCATGCAATGTTTTATCCTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTC	1320
1321	GATGCAACTTATCAAAAGAATATCTCAATACAGAATCTCAAGTAATTCGTGACAGGCAAT	1380
1321	GATGTAACTTATCAGAAAGAATATCTCAATACAGAATCTCAAGTAATTAATTAACAGGCAAT	1380

QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCACCACTCGATAGTAAGTAATGCTTTAGATAAG 1440
DB 1381 CTTGATATCTCAACTGAGCTTGGGAATGTCACCACTCGATAGTAAGTAATGCTTTAGATAAG 1440
QY 1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCACATCCGCT 1500
DB 1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCACATCTGCT 1500
QY 1501 CTCATCAGCTATATGTTTTAACTGTCAATATCTCTGTTTGTGGTATATCTTAGCCTGGTT 1560
DB 1501 CTCATTACCTATATGTTTTGACTATCATATCTCTGTTTGTGGTATATCTTAGCCTGATT 1560
QY 1561 CTAGCATCTACCTGATGTACAAGCAAAAGGCGCAACAGAGACCTTGTATGGCTTGG 1620
DB 1561 CTAGCATCTACCTGATGTACAAGCAAAAGGCGCAACAGAGACCTTGTATGGCTTGG 1620
QY 1621 AATTAATACCTGGATCAGATGAGAGCCACTAGAAAATGTGA 1662
DB 1621 AATAATACCTGATCAGATGAGAGCCACTACAAAATGTGA 1662

RESULT 9

US-08-804-372A-10
Sequence 10, Application US/08804372A
Patent No. 6183753
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,372A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2552/39115E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1662

US-08-804-372A-10

Query Match 85.0%; Score 1412.4; DB 3; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGATGCTGACCGTCCGGTCCGG 60
DB 1 ATGGGCTCCAGACCTTCTACCAAGAACCCAGCACTTATGATGCTGACTATCCGGGTCGG 60
QY 61 CTGGCAGTCTGAGTCTGCTGCTCCGACAGCTCCCTTGTATGCGAGCCCTCTTGCAGCTGCA 120
DB 61 CTGGTACTGAGTCTGCTGCTCCGGCAAACTCCATTTGATGGAGGCCCTCTTGCAGCTGCA 120
QY 121 GGGATTGTGGTGAAGGAGACAAAGAGCTCAACATATACACCTCATCTCAGACAGGGTCA 180
DB 121 GGAATTTGGTGTACAGGAGACAAAGAGCTCAACATATACACCTCATCTCAGACAGGATCA 180
QY 181 ATCATAGTCAAGTTTACTCCCAATATGCCAAAGATTAAGAGGCGTGTGCAAAAGCCCG 240
DB 181 ATCATAGTTAAGTCTCTCCCAATCTGCCAAAGATTAAGAGGCGATGTGCAAAAGCCCG 240
QY 241 TTGGAGGCGTCAACAGAGACATTGACTACTTTTGTCTCACCCCTTGGTGTATTTCTTTCGT 300
DB 241 TTGGATGCATACAAACAGAGACATTGACCACTTTTGTCTCACCCCTTGGTGTATTTCTTTCGT 300
QY 301 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTTATGGCGCC 360
DB 301 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTTATGGCGCC 360
QY 361 ATTATCGCGGTGAGCTCTCGGGGTTGCAACCGCTGCACAGATAACAGAGAGCTTCGGCT 420
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QY 421 CTGATACAGCCAAACCAAAATGCTGCCAACTCTCGGGCTTAAAGAGAGAAATGCTGCA 480
DB 421 CTGATACAGCCAAACCAAAATGCTGCCAACTCTCGGGCTTAAAGAGAGCAATGCGCGCA 480
QY 481 ACCAATGAGCTGTGCAGAGTCACTGATGAGATTATCAAACTAGCAGTGGCAGTTGGG 540
DB 481 ACCAATGAGCTGTGCAGAGTCACTGATGAGATTATCGAAGATTATCGAAGTGGCAGTTGGG 540
QY 541 AAGATGCAAGCAATTTGTTAATGACAGCTTTAATAAAGCAGCTCAGGAATTCGACTGTATA 600
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DB 781 AGCTCAATTAATTTGGTAGCGGCTTAAATCAACCGGTAACTTCTATACGACTCAGACT 840
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DB 841 CAATCTTGGGTATACAGTAACTTCTACCTTCACTCGGGAACCTTAAATAATATCGTGC 900
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DB 1021 ACTGACTTAGATTTATATTGTGACAGAAATAGTAAGTTCCCTATGTCCCTGTTTAT 1080


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QY 1081 TCCTGTTTGGGCGCAATACATCGGCTTGCATGTACTCGAAGACTGAAGCGCACTCACT 1140
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DB 1201 TGTGTAAGCCCCCGGTTATCATATATCGAAAAATATGGAAGAGCTGTCTCTAATAGAT 1260
QY 1261 AGGCATCATGAATCTCTATCTCTTAGACGGAATTAATTTAGGCTCAGTGGGAATTT 1320
DB 1261 AAACAATCATGAATCTCTATCTCTTAGACGGAATTAATTTAGGCTCAGTGGGAATTT 1320
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QY 1561 CTAGCATGCTACGTATGTAACAGAAAAGCGCGCAACAGAAATGGA 1662
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RESULT 10

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PCT-US95-10245-12
; Sequence 12, Application PC/TUS9510245
; GENERAL INFORMATION:
; APPLICANT: SYNTRO CORPORATION
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10245
; FILING DATE: 09-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1662
; PCT-US95-10245-12
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Query Match 85.0%; Score 1412.4; DB 5; Length 1662;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATGGGCTCCAGATCTTTCTACAGGATCCAGATACCTCTCTGATGTGACCGTTCGGGTCGG 60
DB 1 ATGGGCTCCAGATCTTTCTACAGGATCCAGATACCTCTCTGATGTGACCGTTCGGGTCGG 60
QY 61 CTGGCTCTAGTTCGTCTGTCGCAAGCTCCCTTGATGGCAGGCTCTTGCAGTCA 120
DB 61 CTGGTACTAGTTCGTCTGTCGCAAGCTCCCTTGATGGCAGGCTCTTGCAGTCA 120
QY 121 GGGATTGTGTCAGAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
DB 121 GGAATTGTGTTACAGGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
QY 181 ATCATAGTCAAGTTACTCCCAATATGCCCCAAGATAAAGAGCGGTGTGCAAAAGCCCCG 240
DB 181 ATCATAGTTAAGTCTCTCCGAATCTGCCAAAGGATAAGGAGGCATGTGCAAAAGCCCC 240
QY 241 TTGGAGGCGTACACAGGACATGTACTTGTCTCACCCTTGGTGATTTCTATTCGT 300
DB 241 TTGGATGTCATCAACAGGACATTTGACCACTTTGCTCACCCCTTGGTGACTCTATCCGT 300
QY 301 AGGATACAGAGTCTGTGACTACATCTGAGAGAGGAGAAACAGGAGCGCTTATAGCGCC 360
DB 301 AGGATACAGAGTCTGTGACTACATCTGAGAGGAGGAGACAGGAGCGCTTATAGCGCC 360
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DB 361 ATTATTCGGCGTGTGCTCTCTGCGGTTCGCACTGCGCAAAATAACAGCGCGCGAGCT 420
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DB 421 CTGATACAGCCAAACCAAAATGCTGCAACATCTCTCGGCTTAAAGAGAGAAATGTGCA 480
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DB 481 ACCAATGAGGCTGTGATGAGGTCACTGCGGATTAATCGCAATTCGCACTAGCAGTGGG 540
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DB 601 AAAATTGCAAGCAAGTTGCTGTAGAACTCAACCTGTATCTAATCTGAATGACTACAGTA 660
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DB 661 TTGGGCGCAAAATCACTTCCCTGCTTAAACCCAGCTGACTATCAGGCGCTTTTCAAT 720
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DB 721 CTAGCTGGTGGGAATATGGAATTAATTTGACTAAGTTAGGTAGGTAGGGAACCAACTC 780
QY 781 AGCTCAATTAATGTTAGGCGCTGATCAACCGCAACCTTCTTCTGACGCTCAGAGCT 840
DB 781 AGCTCAATTAATGTTAGGCGCTTAAATCAACCGGTAACCTTCTTCTGACGCTCAGAGCT 840
QY 841 CAGCTCTGGGTATACAGGTAAACCTTACCTCAGTCGGGAACCTGAATATATATGCGTGCC 900
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Db 841 CAACCTCTGGGTATACAGTAACCTCTACCTTCAGTCGGGAACCTAAATAATATGCGTCC 900
Qy 901 ACCTACTTGGAAACCTCTCTGTAGTACACCAAGGATTTGCTCAGCACTGCTCCCA 960
Db 901 ACCTACTTGGAAACCTTATCCGTAAAGCAACACGAGGATTTGCTCAGCACTTGTCCCA 960
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Db 1021 ACTGACTTAGATTTATATTTGTAAGAAGATAGTAAAGTTCCCTATGCTCCTGGTATTTAC 1080
Qy 1081 TCCTGTTTGGCGGCAATACATCGCTTGCATGTAAGTCTGGAAGTGAAGGGCACTCACT 1140
Db 1081 TCCTGCTTGGCGGCAATACATCGCTTGCATGTAAGTCTGGAAGTGAAGGGCACTTACT 1140
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Db 1201 TGTGTAACCCCGGGTATCATATCGCAAAATTTATGAGAAGTGTGTCTCTAATAGAT 1260
Qy 1261 AGGCAATCATGATGCTCTATCTTACACGGAATTTGAGGCTCAGTGGGGAATTT 1320
Db 1261 AAACAATCATGATGTTTATCTTATCTTAGCGGGATTAATTTAAGGCTCAGTGGGGAATTC 1320
Qy 1321 GATGCAACTTATCAAAAAGATATCTCAATACAGATTTCTCAAGTAATCGTGACAGGCAAT 1380
Db 1321 GATGTAACCTATCAGAGAATATCTCAATACAGATTTCTCAAGTAATTAATTAAGGCAAT 1380
Qy 1381 CTCGATATCTCGATGAGCTTGGGAATGCAAACTCGATCAAGTAACTGTAAGTAACTTATAGATAAG 1440
Db 1381 CTTGATATCTCAACTGAGCTTGGGAATGCAAACTCGATCAAGTAACTGTAAGTAACTTGAATAAG 1440
Qy 1441 TTAGAGGAAGCAACAGCAACTAGCAAGTCAATGTCAACTGTAAGTAACTGTAAGTAACTTGAATAAG 1500
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Qy 1501 CTCATCACCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560
Db 1501 CTCATTAACCTATATCGTTTAACTGTCTATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560
Qy 1561 CTAGCATGCTTACCTGATGTAAGCAAAAGCGGCAACAGAGAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620
Db 1561 CTAGCATGCTTACCTGATGTAAGCAAAAGCGGCAACAGAGAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620
Qy 1621 AATAATACCTGATGATGAGAGGCACTACGAAATGTGA 1662
Db 1621 AATAATACCTGATGATGAGAGGCACTACGAAATGTGA 1662
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RESULT 11

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US-08-484-575A-12
Sequence 12, Application US/08484575A
Patent No. 5926358
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran and David E. Junker
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 115..1860
FEATURE:
NAME/KEY: CDS
LOCATION: 2095..3756
US-08-484-575A-12
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Query Match 85.0%; Score 1412.4; DB 2; Length 4177;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Qy 61 CTGGCACTGAGTTCGGTCTGTCGCAAGCTCCCTGATGCGAGCCCTTTGCACTGCA 120
Db 2155 CTGGTACTGAGTTCGATCTGTCGGCAAACTCCATTTGATGCGAGCCCTTTGCACTGCA 2214
Qy 121 GGGATTGTGTGACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 180
Db 2215 GGAATTGTGTTACAGGAGCAAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 2274
Qy 181 ATCATAGTCAAGTTCCTCCAAATATATGCCAAAGATAAAGAGCGGTGTGCAAAAGCCCGC 240
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QY 1621 AATAATACCTGTATGATGAGAGCCACTACGAAATGTGA 1662
Db 3715 AATAATACCTGTATGATGAGAGCCACTACGAAATGTGA 3756
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RESULT 12

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US-08-477-459-12
; Sequence 12, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
; US-08-477-459-12
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Query Match 85.0%; Score 1412.4; DB 3; Length 4177;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 ATCGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGTGACCGTCCGGGTGCG 60
Db 2095 ATGGGCTCCAGACTTCTACCAAGAACCCAGCACTATGATGCTGACTATCCGGGTGCG 2154
QY 61 CTGGCACTGAGTTGCTGTCTGTCGACAGCTCCCTTGATGGCAGGCTCTTGACGTGCA 120
Db 2155 CTGGTACTGAGTTGCACTCTGTCGCGCAAACTCCATTTGATGGCAGGCTCTTGACGTGCA 2214
QY 121 GGGATTGTGTGACAGGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTCA 180
Db 2215 GGAATTTGTTACAGAGACAAAGCAGTCAACATATACACCTCATCCAGACAGATCA 2274
QY 181 ATCATAGTCAAGTTACTCCCAATATATGCCAAAGATAAGAGCGGTGTGCAAAAGCCCCG 240
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QY 241 TTGGAGCGGTACAAAGGACATTTGACTACTTGTGCTACCCCCCTTGGTGTATTCTTCT 300
Db 2335 TTGGATGTCATACAAAGGACATTTGACTACTTGTGCTACCCCCCTTGGTGTATTCTTCT 2394
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2995 ACCTACTTTGGAACCTTATCGTAAGCACACCGAGGATTTGCTCAGCACTCGTCCCA 3054
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3055 AAAGTGTGTATGAAGTGTGGTTCGTGTATGAAGAACTTGACCTCTACTGTATAGAG 3114
1021 ACCGATTTGGATCTATATTTGTAAGAATAGTGAATTCCTATGTCTCTGGTATTTAT 1080
3115 ACTGACTTAGATTTATATTTGTAAGAATAGTGAATTCCTATGTCTCTGGTATTTAT 3174
1081 TCCTGTTTGGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAGGCGCACTCACT 1140
3175 TCCTGTTTGGCGGCAATACATCGGCTTGCATGTACTCGAAGACTGAGGCGCACTCACT 3234
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3235 ACACCATATGACTATCAAGGCTCAGTCTCGTAACTGCAAGATGACAACTGTAGA 3294
1201 TGTGACAGCCCGGGGTATCATATCGCAAAATTTATGAGAGAGCTGTCTCTAATAGAT 1260
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1261 AGGCAATCATGATGTCTCTATCTTTAGACGGAATACTTTGAGGCTCAGTGGGGAATTT 1320
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1621 AATTAATACCTGATGTCAAGCAAAAGCGCAACAGAGACTTGTGTTATGCTTGGG 1662
3715 AATTAATACCTGATGTCAAGCAAAAGCGCAACAGAGACTTGTGTTATGCTTGGG 3756

RESULT 13

US-08-479-869-12
; Sequence 12, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 115..1860
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2095..3756
US-08-479-869-12

Query Match 85.0%; Score 1412.4; DB 3; Length 4177;

Best Local Similarity 90.6%; Pred. No. 0; Mismatches 156; Indels 0; Gaps 0;

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QY 2095 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACATATCCGGGTGGG 2154
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QY 2155 CTGGTACTGATGTGCACTCTGTCGGCAACTCCATTGATGGCAGGCTCTTGTGAGTGTGA 2214
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QY 2215 GGAATGTGTGTGACAGAGACAAAGCAGTCAAAATATACATATACATCTATCTACAGAGGTGA 2274
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QY 1561 CTGATCACTATATCGTTTAACTGTATATCTCTTGTGTTGTTGTTATAGCTTGGT 1620
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QY 1621 AATAATACCTCGATCAGATGAGGCACTTACGAAATGTGA 1662
Db |||||
QY 3715 AATAATACCTCGATCAGATGAGGCACTTACGAAATGTGA 3756
Db |||||
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RESULT 14

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US-08-486-414-12
; Sequence 12, Application US/08486414B
; Patent No. 6136318
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
; FILE REFERENCE: 42771D
; CURRENT APPLICATION NUMBER: US/08/486,414B
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4177
; TYPE: DNA
; ORGANISM: Fowlpox virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(1857)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2095)..(3753)
; US-08-486-414-12
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Query Match 85.0%; Score 1412.4; DB 3; Length 4177;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
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QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGATACCTTCTGATGCTGACCGGTGGG 60
Db |||||
QY 2095 ATGGGCTCCAGATCTTCTACAGGATCCAGATACCTTCTGATGCTGACCGGTGGG 2154
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RESULT 15
PCT-US94-01826A-12
; Sequence 12, Application PC/TUS9401826A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-PPV-043 and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO


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Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1452.4	87.4 1662 9	US-09-784-990-10 Sequence 10, Appl
2	1452.4	87.4 1662 14	US-10-229-412-10 Sequence 10, Appl
3	1431.6	86.1 15882 12	US-10-440-419-56 Sequence 56, Appl
4	1417.2	85.3 15900 12	US-10-440-419-55 Sequence 55, Appl
5	1412.4	85.0 15186 10	US-09-741-744A-134 Sequence 134, Appl
6	1412.4	85.0 15186 14	US-10-377-718-3 Sequence 3, Appl
7	1412.4	85.0 15186 15	US-10-429-735-3 Sequence 3, Appl
8	1375.4	82.8 3570 9	US-09-881-457A-1 Sequence 1, Appl
9	162.2	9.8 15492 9	US-09-733-692A-60 Sequence 60, Appl
10	162.2	9.8 15498 9	US-09-733-692A-62 Sequence 62, Appl
11	162.2	9.8 15498 9	US-09-733-692A-61 Sequence 61, Appl
12	92.8	5.6 1986 12	US-10-670-695-35 Sequence 35, Appl
13	92.8	5.6 2113 10	US-09-951-061A-86 Sequence 86, Appl
14	92.8	5.6 4343 10	US-09-951-061A-91 Sequence 91, Appl
15	92.8	5.6 4604 10	US-09-951-061A-93 Sequence 93, Appl

16	87.8	5.3	692	14	US-10-206-901B-50	Sequence 50, Appl
17	84.2	5.1	2384	15	US-10-397-635-8	Sequence 8, Appl
18	82.6	5.0	1653	9	US-09-873-233A-17	Sequence 17, Appl
19	81	4.9	1653	9	US-09-873-233A-19	Sequence 19, Appl
20	56.2	3.4	15456	10	US-09-900-112-35	Sequence 35, Appl
21	56.2	3.4	15456	10	US-09-900-112-36	Sequence 36, Appl
22	40.4	2.4	1620	15	US-10-371-264-25	Sequence 25, Appl
23	40.4	2.4	1620	15	US-10-371-099-321	Sequence 321, Appl
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30	39.2	2.4	1620	15	US-10-371-264-23	Sequence 23, Appl
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35	39.2	2.4	13215	15	US-10-371-099-20	Sequence 20, Appl
36	39.2	2.4	13215	15	US-10-371-122-20	Sequence 20, Appl
37	39.2	2.4	13215	15	US-10-373-567-96	Sequence 96, Appl
38	38.2	2.3	8726	9	US-09-070-927A-95	Sequence 95, Appl
39	38	2.3	811	14	US-10-184-644-414	Sequence 414, Appl
40	38	2.3	811	14	US-10-184-634-414	Sequence 414, Appl
C 41	38	2.3	950	12	US-10-027-632-258267	Sequence 258267, Appl
C 42	38	2.3	950	12	US-10-027-632-258268	Sequence 258268, Appl
C 43	38	2.3	950	12	US-10-027-632-258269	Sequence 258269, Appl
C 44	38	2.3	950	12	US-10-027-632-258270	Sequence 258270, Appl
C 45	38	2.3	950	12	US-10-027-632-258271	Sequence 258271, Appl

ALIGNMENTS

RESULT 1

US-09-784-990-10
; Sequence 10, Application US/09784990
; Patent No. US20020037292A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/09/784,990
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-09-784-990-10

Query Match	87.4%	Score 1452.4;	DB 9;	Length 1662;	
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QY 1261 AGGCAATCATCAATGTCTCTATCTTAGACGGATAAATCTTTAGGCTCAGTGGGAATTT 1320
Db 1261 AGGCAATCATCAATGTCTCTATCTTAGACGGATAAATCTTAGGCTCAGTGGGAATTT 1320
QY 1321 GATGCAACTTATCAAAAGATATCTCAATACAGATTCTCAAGTAAATCGTGACAGGCAAT 1380
Db 1321 GATGCAACTTATCAAAAGATATCTCTATATCTAGATTCTCAAGTATATAGTACAGGCAAT 1380
QY 1381 CTCGATATCTCGACTGAGCTTTGGGAATCTCAAACTCTCAAACTGATGCTTTAGTAAG 1440
Db 1381 CTCGATATCTCAACTGAGCTTTGGGAATCTCAAACTCTCAAACTGATGCTTTAGTAAG 1440
QY 1441 TTAGAGGAAGCAACAGCAGCAATAGACAAAGTCAATGTCAAACTGACAGCAGATCCGCT 1500
Db 1441 TTAGAGGAAGCAACAGCAGCAATAGACAAAGTCAATGTCAAACTGACAGCAGATCTGCT 1500
QY 1501 CTCATCACTATATGCTTTTAACTGTCTATCTCTTTGTTGTTGTTATCTTAGCCTGGT 1560
Db 1501 CTCATCACTATATGCTTTTAACTGTCTATCTCTTTGTTGTTGTTATCTTAGCCTGGT 1560
QY 1561 CTAGATGCTACTGATGTACAAGCAAAAGGCGCAAGAGACCTTTGTTAGCTTGGG 1620
Db 1561 CTAGATGCTACTGATGTACAAGCAAAAGGCGCAAGAGACCTTTGTTAGCTTGGG 1620
QY 1621 AATAATACCTGGATCAGATGAGAGCCACTACGAAATGTGA 1662
Db 1621 AATAATACCTGGATCAGATGAGAGCCACTACGAAATGTGA 1662

RESULT 2

US-10-229-412-10
; Sequence 10, Application US/10229412
; Publication No. US20030124145A1
; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE
; APPLICANT: BOUCHARDON, ANNABELLE
; APPLICANT: RIVIERE, MICHEL
; TITLE OF INVENTION: AVIAN POLYNUCLEOTIDE VACCINE FORMULA
; FILE REFERENCE: 454313-2260
; CURRENT APPLICATION NUMBER: US/10/229,412
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US/09/232,479
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 96/09339
; PRIOR FILING DATE: 1996-07-19
; PRIOR APPLICATION NUMBER: PCT/FR97/01326
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Newcastle disease virus
US-10-229-412-10

Query Match 87.4%; Score 1452.4; DB 14; Length 1662;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1531; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACTCTGTAGCTGACCGTCCGGTCCGCG 60
Db 1 ATGGGCTCCAGATCTTCTACAGGATCCCGGTACTCTTAATGCTGATCATCCGAACCCG 60
QY 61 CTGGCAGTGGTGGTCTGTCGACAGCTCCCTTGTAGTGGCAGGCTCTTTCAGCTGCA 120
Db 61 CTGGCAGTGGTGGTCTGTCGACAGCTCTCTTGTAGTGGCAGGCTCTTTCAGCTGCA 120
QY 121 GGGATTTGGTGTGACAGGAGCAAAAGCAGTCAACATATACACTCATCTCAGACAGGTC 180
Db 121 GGGATTTGGTGTGACAGGAGTAAAGCAGTCAACATATACACTCATCCAGACAGGTC 180
QY 181 ATCATAGTCAAGTTACTCTCCCAATATATGCCCAAGATAAAGAGGCGTGTGCAAAAGCCCG 240

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Db 181 ATCATAGTTAAGTTACTCCGGAATATGCCAAGAGCAAAAGAGGTGTGCAAAAGCCCCA 240
Qy 241 TTGAGGCGTACAAAGAGCAATGACTACTTTGCTCACCCCTTGGTGATTTCTATTGCT 300
Db 241 TTGAGGCGTACAAAGAGCACTGACTACTTTACTCACCCCTTGGTGATTTCTATTGCT 300
Qy 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGACGCTTATAGGCGCC 360
Db 301 AGGATACAAGAGTCTGTGACTACTTTCCGAGGAGGAGACAGACGCTTATAGGTCGC 360
Qy 361 ATTATCGGCGTGCAGCTCTCGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
Db 361 ATTATCGGCGTGTAGCTCTCGGGTTGCGACAGCTGCACAGATAACAGCAGCTTCGGCT 420
Qy 421 CTGATACAAGCAACCAAAATGTCGCAACATCTCCGGCTTAAAGAGAGAAATGCTGCA 480
Db 421 CTGATACAAGCAACCAAGATGCTGCCAACATCTCCGGCTTAAAGAGAGCAATGCTGCA 480
Qy 481 ACCAATGAGCTGTGCAGAGTCACTGATGGATTATCAACACTAGCAGTGGCAGTTGGG 540
Db 481 ACCAATGAGCTGTGCAGAGTCACTGATGGATTATCAACACTAGCAGTGGCAGTGGG 540
Qy 541 AAGATGACGCAATTTGTTAATGACAGTTTAAATAAAACAGCTCAGGAATTTGGACTGTATA 600
Db 541 AAGATGCAACAGTTTGTCAATGACCACTTCAATAATACAGCGCAAGATTTGGACTGTATA 600
Qy 601 AAAATTACCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAATGTAATGACTACAGTA 660
Db 601 AAAATTGACAGCAGGTCGGTGTAGAACTCAACTGTGTACCTAACTGAATTTGACTACAGTA 660
Qy 661 TTGGGGCCAAATCACTCCCTGCTTAAACAGCTGACTATCCAGGCGCTTTACAAT 720
Db 661 TTGGGGCCAAATCACTCCCTGCTTAACTCAGCTGACTATCCAGGCGCTTTACAAT 720
Qy 721 CTAGCTGGTGGGAATATGGAATTTCTGTGACTAAGTTAGTGTAGGGAACAACCAACTC 780
Db 721 CTAGCTGGTGGTAATATGGAATTTCTGTGACTAAGTTAGTGTAGGGAACAACCAACTC 780
Qy 781 AGCTCATTAATTGTTAGCGGCTGATCACCGGCAACCCCTATTTCTGTACGACTCACAGACT 840
Db 781 AGCTCATTAATTGTTAGCGGCTTGTATCAACCAACCAAGGATTTGCTTACGACTCACAGACT 840
Qy 841 CAGCTCTTGGGTATACAGGTAAACCTACCTCAGTCGGGAACCTGATATATGCGTGCC 900
Db 841 CAGATCTTGGGTATACAGGTAACTTTGCTTCACTGGGAACCTGATATATGCGTGCC 900
Qy 901 ACCTACTTGGAAACCTTGTCTGTAAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Db 901 ACCTACTTGGAGACTTATCTGTAAGTACAAACCAAGGATTTGCTCAGCACTGTGCCA 960
Qy 961 AAGGTGTGTATGAGTGGTTCGGTGTATGAGAACTTGACACCTCATCTGATATAGAG 1020
Db 961 AAGGTGTGTATGAGTGGTTCGGTGTATGAGAACTTGACACCTCATCTGATATAGG 1020
Qy 1021 ACCGATTTGATCTATATTTGTAAGATAGTGCATTCCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 ACCGATTTGATTTATCTGTAAGATAGTGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Qy 1081 TCCTGTTTGGCGCAATATACCTGCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 TCCTGTTGAGCGGTAATATACCTGCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Qy 1141 ACGCCGTATATGACTCTCAAGGCTGATGTTATGCGCAACTGTGATGATGACATGATGATG 1200
Db 1141 ACGCCATATATGCTCTCAAGGCTGATGTTATGCGCAACTGTGATGATGATGATGATGATG 1200
Qy 1201 TGTGCAGACCCCGGGTATCATATCGCAAAATTTATCGAGAGCTGTGCTCTTAATAGAT 1260
Db 1201 TGTGCAGATCCCCAGGTATCATATCGCAAAATTTATCGAGAGCTGTGCTCTTAATAGAT 1260
Qy 1261 AGGCAATCATGCAATGCTTATCTTATAGCGGAATATCTTTGAGGCTCAGTGGGGAATTT 1320
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Db 1261 AGGCACTCATGCAACGCTTCTTATCCTTAGACGGGATAAATCTTGAGGCTCAGTGGGGAATTT 1320
Qy 1321 GATGCAACTTTATCAAAAGAAATATCTCAATACAAAGATTCTCAAGTAATCTGACAGGCAAT 1380
Db 1321 GATGCAACTTATCAAAAGAAATATCTCTATATAGTATCTCAAGTTATAGTGACAGGCAAT 1380
Qy 1381 CTGATATCTCGACTGAGCTTGGGAATGTCAACNACTCGATAGTAAATGCTTTAGATAG 1440
Db 1381 CTTGATATATCAACTGAGCTTGGGAATGTCAACNACTCAATAAGTAATGCTTGAATAAG 1440
Qy 1441 TTAGAGAAAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACTGACACAGCACATCGCT 1500
Db 1441 TTAGAGAAAAGCAACAGCAAACTAGACAAGGTCAATGTCAAACTGACACAGCACATCTGCT 1500
Qy 1501 CTCAATCACTTATATCGTTTAACTGTCAATATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
Db 1501 CTCAATCACTTATATCGTTTAACTGTCAATATCTCTTGTGTTGTTGTTGTTGTTGTTGTT 1560
Qy 1561 CTAGCATGCTACCTGATGTACAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGG 1620
Db 1561 CTAGCATGCTACCTGATGTACAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGG 1620
Qy 1621 AATAAATACCTTGGATCAGATGAGAGCCACTACGAAAATGTGA 1662
Db 1621 AATAAATACCTTGTATGATGAGAGCCACTACAAAATATGA 1662
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RESULT 3

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US-10-440-419-56
; Sequence 56, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 15882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-56
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Query Match 86.1%; Score 1431.6; DB 12; Length 15882;
Best Local Similarity 91.3%; Pred.No. 0;
Matches 1518; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCAGATCTTCTACCAAGATCCCAAGTACCTCTGATGTGACCGTCCGGGTCGCG 60
Db 4544 ATGGGCCCCAGACCTTCTACCAAGAACCCAGTACCTATGATGCTGACTGCTCCAGTCCG 4603
Qy 61 CTGGCACTGAGTTGCTGCTGTCGCAAAAGCTCCCTTGTAGTGAGGAGGCTCTTTCAGCTGCA 120
Db 4604 CTGGTACTGAGTTGCTGCTGTCGCGCAAACTCCATTTGATGGCAGGCTCTTTCGGGCTGCA 4663
Qy 121 GGGATTTGGTGTACAGGACGACAAAGCAAGCTCAACATATACACCTCATCTCAGACAGGTC 180
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4664 GGAATTGGTAAACAGGAGACAAAGCAGTCAACATATACACTCATCCAGACAGGATCA 4723
181 ATCATAGTCAAGTTACTCCCAATAATGCCCCAAGATAAAGAGGCGTGTGCAAAAGCCCG 240
4724 ATCATAGTTAAGTCTCTCCCAACCTGCCCAAGGATAAGAGGCGATGTGCGAAAGCCCCC 4783
241 TTGGAGGCGTCAACAGGACATTTGACTCTTTGCTTCAACCCCTTTGGTGTATTCTATTGCT 300
4784 TTGGATGATACACAGACATTTGACCACTTTGCTTCAACCCCTTTGGTGTACTCTATCCGT 4843
301 AGGATCAAGAGTGTGATCATCTCTGGAGAGGGAACAGGAGCGCTTATAGGCGCC 360
4844 AGGATCAAGAGTGTGATCATCTCTGGAGGAGGAGACAGAAACGCTTTATAGGCGCC 4903
361 ATTATCGGCGGTGAGCTCTCGGGGTGCAACCGGTGACAGATTAACAGCAGTTTGGCT 420
4904 ATTATCGGCGGTGAGCTCTCGGGGTGCAACCGGTGCAACCGGTGCAACCGGTGCAACCG 4963
421 CTGATCAAGGCAACCAAAATGCTGCCAACATCTCTCGGCTTTAAAGAGAGAAATTCCTGCA 480
4964 CTGATCAAGGCAACCAAAATGCTGCCAACATCTCTCGGCTTTAAAGAGAGCAATTCGCCGA 5023
481 ACCAATGAGGTGTGCAAGAGTCACTGATGANTATCAAACTAGAGTGTGCAAGTGGG 540
5024 ACCAATGAGGCGTGCATGAGTCACTGACGATTTATCGCAACTAGCAGTGTGCAAGTGGG 5083
541 AAGATGACGCAATTTGTTAATGACCAAGTTTAAATAAACAGCTCAGGAATTTGACGTGATA 600
5084 AAGATGACGCAATTTGTTAATGACCAAGTTTAAATAAACAGCTCAGGAATTTGAGCTGCAATC 5143
601 AAAATTAACCCAGCAGTGTGGTGTAGAACTCAACCTGTGTATCAACTGAATTTGACTACAGTA 660
5144 AGAATTCACAGCAAGTGTGGTGTAGAGTCAACCTGTACCTTAACCGAATTTGACTACAGTA 5203
661 TTCGGGCCAACAATCACTTCCCTGCTTAAACCAAGCTGACTATTTACAGCAGTTCACAACT 720
5204 TTCGGGCCAACAATCACTTCCCTGCTTAAACCAAGCTGACTATTTACAGCAGTTCACAACT 5263
721 CTAGCTGTGGGAATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 780
5264 CTAGCTGTGGGAATATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 5323
781 AGCTCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 840
5324 AGCTCAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 5383
841 CAGCTCTTGGGTATACAGTAACCTTACCTCAGTCGGGAACCTGAAATAATGCGTGGC 900
5384 CAACTCTTGGGTATACAGTAACCTTACCTCAGTCGGGAACCTGAAATAATGCGTGGC 5443
901 ACCTACTTGGAAACCTTCTGTGTAAGTACACCAAGAGATTTGCTCAGCAGCTCGTCCCA 960
5444 ACCTACTTGGAAACCTTCTGTGTAAGTACACCAAGAGATTTGCTCAGCAGCTCGTCCCA 5503
961 AAGTGTGTGATGAAGTGTGGTTCGTGTGATGAAGAACTTGACACCTCATCTGTATAGAG 1020
5504 AAGTGTGTGATGAAGTGTGGTTCGTGTGATGAAGAACTTGACACCTCATCTGTATAGAG 5563
1021 ACCGATTTGGATCTATATGATACAGATAGTGAATTCCTTATGCTCTGCTGGTATTAT 1080
5564 ACCGATTTGGATCTATATGATACAGATAGTGAATTCCTTATGCTCTGCTGGTATTAT 5623
1081 TCCTGTTTGGAGGCAATACATCGGCTGTGATGATCGAAGCTGAAGGCGCACTCACT 1140
5624 TCCTGTTTGGAGGCAATACATCGGCTGTGATGATCGAAGCTGAAGGCGCACTCACT 5683
1141 ACGCGGTATACATCTCTCAAGGCTCAGTTATTGCGAACTGTGAAGATGACAACTGTAGA 1200
5684 ACGCGGTATACATCTCTCAAGGCTCAGTTATTGCGAACTGTGAAGATGACAACTGTAGA 5743
1201 TGTGACAGCCCCCGGTATCATATCGGAATTTATGAGAGAGCTGTCTCTAATAGAT 1260
5744 TGTGTAACCCCCCGGTATCATATCGGAATTTATGAGAGAGCTGTCTCTAATAGAT 5803

1261 AGGCAATCATGCAATGCTCTATCCTTTAGACGGAATAAATCTTTAGGCTCAGTGGGAATTT 1320
5804 AAGCAATCATGCAATGCTTTTATCCTTTAGACGGAATAAATCTTTAGGCTCAGTGGGAATTT 5863
1321 GATGCAATCTTCAAAAGATATCTCAATACAAAGATTTCTCAAGTAAATCGTGCAGGCAAT 1380
5864 GATGCAATCTTCAAAAGATATCTCAATACAAAGATTTCTCAAGTAAATTAATACAGCAAT 5923
1381 CTCGATATCTGATGAGCTTTGGGAATGTCAAACTCGATAAGTAATGCTTTGATTAAG 1440
5924 CTTGATATCTCAATGAGCTTTGGGAATGTCAAACTCGATCAAGTAAATGCTTTGATTAAG 5983
1441 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCAATCCGCT 1500
5984 TTAGAGGAAGCAACAGCAAACTAGACAAAGTCAATGTCAAACTGACCAAGCAATCTGCT 6043
1501 CTCATCACTATATGCTTTTAACTGTCTATATCTCTTTGTTGTTGTTATCTTAGCCTGGTT 1560
6044 CTCATCACTATATGCTTTTAACTGTCTATATCTCTTTGTTGTTGTTATCTTAGCCTGGTT 6103
1561 CTAGATCTTACCTGATGTACAAGCAAAAGGCGCAAGAGACCTTTGTTGCTTGGG 1620
6104 CTAGATCTTACCTGATGTACAAGCAAAAGGCGCAAGAGACCTTTGTTGCTTGGG 6163
1621 AATATACCTTGGATCAGATCAGAGGCACTACGAAATGTGA 1662
6164 AATATACCTTGGATCAGATCAGAGGCACTACGAAATGTGA 6205

RESULT 4

US-10-440-419-55
; Sequence 55, Application US/10440419
; Publication No. US20030224017A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, SIBA K.
; APPLICANT: HUANG, ZHUHUI
; TITLE OF INVENTION: RECOMBINANT NEWCASTLE DISEASE VIRUSES USEFUL AS
; FILE REFERENCE: 108172-00096
; CURRENT APPLICATION NUMBER: US/10/440,419
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/926,431
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/06700
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/381,462
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/171,072
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/132,597
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 55
; LENGTH: 15900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant cDNA for NDV
US-10-440-419-55

Query Match 85.3%; Score 1417.2; DB 12; Length 15900;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1509; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCCGGGTGCGG 60
DB 5258 ATGGGCTCCAGATCTTCTACCAAGAACCCAGCACCTATGCTGCTACTATCCGGGTGCGG 5317
QY 61 CTGGCAGCTGAGTGGCTGTCTCCGACAGCTCCCTTGTGATGGAGCCCTCTTCAGCTGCA 120
DB 5318 CTGGTACTGAGTTGATCTGTCCGGCAAACTCCATTGATGGAGGCGCTCTTCAGCTGCA 5377


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QY 121 GGGATTGTGGTGACAGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGGTCA 180
Db 5378 GGAATTGTGGTTACAGGAGACAAAGCCGTCAACATATACACCTCATCCAGACAGGATCA 5437
QY 181 ATCATAGTCAAGTTACTCCCAAAATATGCCAAAGATAAAGAGGGGTGTGCAAAAGCCCGC 240
Db 5438 ATCATAGTTAAGTCTCTCCGAACTGCCCCAAGATAGAGAGGCATGTGCGAAGCCCCC 5497
QY 241 TTGAGGGGTACACAGGACATTGACTACTTTGTCTACCCGCCCTTGGTGATCTATTGCT 300
Db 5498 TTGATGCATACAAAGGACATTGACCACTTTGTCTACCCGCCCTTGGTGACTCTATCCGT 5557
QY 301 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAAACAGGAGCGCTTATAGGCGCC 360
Db 5558 AGGATACAAGAGTCTGTGACTACATCTGGAGGAGGAGAGCGGCGCTTATAGGCGCC 5617
QY 361 ATTATCGCGCGTGCAGCTCTCGGGGTTGCAACCGCTGCACAGATAAACAGCAGCTTCGGCT 420
Db 5618 ATTATCGCGGTGTGGCTCTTTGGGTTGCAACTGCCGCACAAATAACAGCGCGCCAGCT 5677
QY 421 CTGATACAAGCCAAACCAAAATGCTGCCAAGATCTCTCGGCTTAAAGAGAGAAATTGCTGCA 480
Db 5678 CTGATACAAGCCAAACCAAAATGCTGCCAAGATCTCTCGGCTTAAAGAGAGCAATTGCCGCA 5737
QY 481 ACCAATGAGGCTGTGCACGAGGTCACTGATGGATTATCACAACCTAGCAGTGGCAGTTGGG 540
Db 5738 ACCAATGAGGCTGTGCATGAGTCACTGACGGATTATCGCAACTAGCAGTGGCAGTTGGG 5797
QY 541 AAGATGAGCAAAATTTGTAATGACAGTTTAAATAAACAGCTCAGGAATTTGGAAGTATA 600
Db 5798 AAGATGAGCAGGTTTGTATGACCAATTTAATAAAGCAGCTCAGGAATTAGACTGCATC 5857
QY 601 ABAATTACCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAAGTGAATGACTACAGTA 660
Db 5858 ABAATTGACAGCAGGTTGGTGTAGAACTCAACCTGTATCTAAGTGAATGACTACAGTA 5917
QY 661 TTCGGGCGACAAATCACTTCCCTGCCTTAAACCCAGCTGACTATCCAGGGGCTTTACAAT 720
Db 5918 TTCGACCACAAACTCACTTCACTGCTTTAAACAGCTGACTATTCAGGCACTTTACAAT 5977
QY 721 CTAGCTGGTGGGAATATGGATTACTTGTGACTAAGTTAGGTGTAGGGAACAACCAACTC 780
Db 5978 CTAGCTGGTGGAAATATGGATTACTTATGACTAAGTTAGGTGTAGGGAACAATCAACTC 6037
QY 781 AGCTCATTAATTGCTAGCGGCTGATCACCGGCAACCTATTCTGTAGACTACAGACT 840
Db 6038 AGCTCATTAATCGGTAGCGGCTTAATCACCGGTAAACCTTATCTATACGACTACAGACT 6097
QY 841 CAGCTCTTGGGTATACAGGTAAACCTTACCTCAGTCGGAACCTGAATAATATGCGTGC 900
Db 6098 CAACCTTGGGTATACAGGTAACTCTACCTCAGTCGGAACCTGAATAATATGCGTGC 6157
QY 901 ACCTACTTGGAAACCTTATCGTAAAGCAACCAAGGGAATTTGCTCGGCACCTTGTCCCA 960
Db 6158 ACCTACTTGGAAACCTTATCGTAAAGCAACCAAGGGAATTTGCTCGGCACCTTGTCCCA 6217
QY 961 AAGTGTGTATGAGTGGTTCGTTGATAGAGAACTTGACACCTCATCTGATATAGAG 1020
Db 6218 AAGTGTGTATGAGTGGTTCGTTGATAGAGAACTTGACACCTCATCTGATATAGAA 6277
QY 1021 ACCGATTGGATCTATATTGTACAAGAAATAGTGACATTTCCCTATGTCTCTCTGGTATTAT 1080
Db 6278 ACTGACTTAGATTATATTGTACAAGAAATAGTAGTTCCTATGTCCCTCTGGTATTAT 6337
QY 1081 TCCTGTGTGACGCGCAATATACCTGCTTGCATGATCTGAAAGACTGAAGGCGCACTCACT 1140
Db 6338 TCCTGTGTGACGCGCAATATACCTGCTTGCATGATCTGAAAGACTGAAGGCGCACTCACT 6397
QY 1141 ACGCCGTATACGACTCTCAAGGCTCAGTTATTGCGCAACTGTATAGATGACAAATGATGA 1200
Db 6398 ACACCATACGACTCTCAAGGTTTCACTCATGCCAACTGCAGATGACAAATGATGA 6457
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QY 1201 TGTGAGACCCCCCGGGTATCATATCGCAAAATATTATGAGAAAGCTGTGTCTCTAATAGAT 1260
Db 6458 TGTGTAACCCCCCGGGTATCATATCGCAAAATATTATGAGAAAGCTGTGTCTCTAATAGAT 6517
QY 1261 AGGCAATCATGCAATGCTCTATCTTATAGACGGAATTAATTTGAGGCTCAGTGGGAAATTT 1320
Db 6518 AAGCAATCATGCAATGCTCTATCTTATAGGCGGGAATTAATTTAAGGCTCAGTGGGGAATTC 6577
QY 1321 GATCAACTTATCAAAAGAATATCTCAATACAAGATTCTCAAGTAATCTGACAGGCAAT 1380
Db 6578 GATCAACTTATCAAGAATATCTCAATACAAGATTCTCAAGTAATTAATAACAGGCAAT 6637
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACACTCGATAGTAATGCTTTTAGTAAG 1440
Db 6638 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATCAGTAATGCTTTTGAATAAG 6697
QY 1441 TTAGAGAAAGCAACAGCAAACTAGACAGAGTCAATGTCAAACTGACCAAGCACATCCGCT 1500
Db 6698 TTAGAGAAAGCAACAGCAAACTAGACAGAGTCAATGTCAAACTGACCAAGCACATCTGCT 6757
QY 1501 CTATCACTATATCGTTTTAACTGTCAATCTCTTGTGTGTATATCTTAGCCTGGTT 1560
Db 6758 CTCAATTACCTATATCGTTTTGACTATCATATCTCTGTTTTGGTATACTTAGCCTGATT 6817
QY 1561 CTAGCATGCTACCTGTGTACAGCAAAAGCGCAACAGAGACCTTGTATGCGTTGGG 1620
Db 6818 CTAGCATGCTACCTGTGTACAGCAAAAGCGCAACAGAGACCTTATTATGCGTTGGG 6877
QY 1621 AATAAATCCCTGGATCAGATGAGAGCCACTACGAAAATGTGA 1662
Db 6878 AATAAATCCCTAGATCAGATGAGAGCCACTACAAAATGTGA 6919
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RESULT 5
US-09-741-744A-134
; Sequence 134, Application US/09741744A
; Publication No. US20030087417A1
; GENERAL INFORMATION:
; APPLICANT: Peeters, Bernardus
; APPLICANT: de Leeuw, Olav
; APPLICANT: Klaus, Guus
; APPLICANT: Arnoud, Gielkens
; TITLE OF INVENTION: Newcastle Disease Virus Infectious Clones, Vaccines and Diagnost
; CURRENT APPLICATION NUMBER: US/09/741,744A
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/NL99/00377
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus Lasota
US-09-741-744A-134

Query Match 85.0%; Score 1412.4; DB 10; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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QY 1 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGTGACCGTCCGGGTGCG 60
Db 4544 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACCTCTGATGTGACCGTCCGGGTGCG 4603
QY 61 CTGGCACTGAGTTCGCTGTGTCGCAAGCTCCCTTGTATGGCAGGCTCTTTCAGCTGCA 120
Db 4604 CTGGTACTGAGTTCGCTGTGTCGCAAGCTCCCTTGTATGGCAGGCTCTTTCAGCTGCA 4663
QY 121 GGAATTGTGTGACAGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGCTCA 180
Db 4664 GGAATTGTGTGACAGAGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGATCA 4723
QY 181 ATCATAGTCAAGTTACTTCCCAATATGCCCAAGATAAAGAGCGGTGTGCAAAAGCCCCG 240
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Db 4724 ATCATAGTTAAGTCTCCGAACTGCCCAGGATAGAGGAGCATGTGCGAAGGCCCCC 4783
QY 241 TTGGAGGGGTAAACAGGACATTTGACTATTTTGTCTACCCCGCTTGGTGTATCTATTCT 300
Db 4784 TTGGATGATACAAACAGGACATTTGACCACTTTGTCTACCCCGCTTGGTGTATCTATTCT 4843
QY 301 AGGATACAAGAGTCTGTGACTACATCTCGAGAGGAGGAAACAGGAGCGCTTATAGGCGCC 360
Db 4844 AGGATACAAGAGTCTGTGACTACATCTCGAGAGGAGGAGCAAGGCGCGCTTATAGGCGCC 4903
QY 361 ATTATCGCGGTGACGCTCTCGGGGTGCAACCGCTGCACAGATTAACAGAGCTTCGGCT 420
Db 4904 ATTAATGCGGTGTGGCTCTTGGGGTGGCACTGCGGCAAAATTAACAGAGCGCGCAGCT 4963
QY 421 CTGATACAAGCAACCAAAATGCTGCCAATCTCCCGCTTAAAGAGAGAAATTTCTGCA 480
Db 4964 CTGATACAAGCAACCAAAATGCTGCCAATCTCCCGCTTAAAGAGAGCAATTTGCCGCA 5023
QY 481 ACCAATGAGGCTGTGACGAGGTCACTGATGATTTATCACACTAGCAATGCGAGTTGGG 540
Db 5024 ACCAATGAGGCTGTGATGAGGTCACTGACGGAATTTATCGCACTAGCAATGCGAGTTGGG 5083
QY 541 AAGATGACAGCAATTTGTTAATGACCACTTTAATAAAACAGCTCAGGAATTTGACTGTATA 600
Db 5084 AAGATGACAGCAATTTGTTAATGACCACTTTAATAAAACAGCTCAGGAATTTGACTGTATA 5143
QY 601 AAAATTAACAGAGGTTGGTGTAGAACTCAACCTGTATCTAACTGAATTTGACTACAGTA 660
Db 5144 AAAATTTGACAGCAAGTTGGTGTAGAGTCAACCTGTATCTAACTGAATTTGACTACAGTA 5203
QY 661 TTCGGGCGCACAAATCACTTCCCGCTTAAACAGCTCAGCTATCCAGCGCTTTTACAAAT 720
Db 5204 TTCGGGCGCACAAATCACTTCCCGCTTAAACAGCTCAGCTATTTTACGACCTTTTACAAAT 5263
QY 721 CTAGCTGTGGGAATATGATTAATCTTTGATTAAGTGTAGGTAGGGAACCAACCACTC 780
Db 5264 CTAGCTGTGGGAATATGATTAATCTTTGATTAAGTGTAGGTAGGGAACCAATCACTC 5323
QY 781 AGCTCAATTAATTTGGTAGCGGCTGATCAACCGGAAACCTTATTTCTGTACACTCAGACT 840
Db 5324 AGCTCAATTAATCGGTAGCGGCTTAAATCAACCGGAAACCTTATTTCTATACACTCAGACT 5383
QY 841 CAGCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAATAATATGCTGTC 900
Db 5384 CAACCTCTTGGGTATACAGTAACTTACCTCAGTCGGGAACCTGAATAATATGCTGTC 5443
QY 901 ACCTACTTTGGAAACCTTTGTCTGTAAAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 960
Db 5444 ACCTACTTTGGAAACCTTTATCCGTAAAGCAACCAAGGATTTGCTCAGCACTTTGTCGCC 5503
QY 961 AAGGTGGTGTAGAGGTGCGTTCGGTGTAGAGAACTTTGACACCTCATCTATGATAGAG 1020
Db 5504 AAGGTGGTGTAGAGGTGCGTTCGGTGTAGAGAACTTTGACACCTCATCTATGATAGAA 5563
QY 1021 ACCGATTTGGATCTATTTATGTAAGATAGTACATTCCTATGTCTCCTGCTATTTAT 1080
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QY 1141 AGCGGTATACACTCTCAAGGCTCAGTTATGCGCAATTTAGAGTAACTGATGATGATGATA 1200
Db 5684 ACACATATACACTCTCAAGGCTCAGTTATGCGCAATTTAGAGTAACTGATGATGATGATA 5743
QY 1201 TGTGACAGCCCCCGGTATCATATCGCAAAATTTAGGAGAGGCTGTGCTCTAATAGAT 1260
Db 5744 TGTGTAACCCCCCGGTATCATATCGCAAAATTTAGGAGAGGCTGTGCTCTAATAGAT 5803
QY 1261 AGGCAATATGCAATGCTCTATCTTTAGACGGAATACTTTGAGGCTCAGTGGGGAATTT 1320
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Db 5804 AAACAAATCATCAATGTTTTTATCTTTAGGCGGGATAACTTTAAGGCTCAGTGGGGAATTC 5863
QY 1321 GATGCAACTTATCAAAAGAAATATCTCAATACAGATTTCTCAAGTAATCGTGACACGCAAT 1380
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QY 1561 CTAGCATCTACCTGATGTACAAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGT 1620
Db 6104 CTAGCATCTACCTGATGTACAAGCAAAAGCGCAACAGAGACCTTGTATGCTTGGT 6163
QY 1621 AATAATACCTGGATCAGATGAGAGCCCACTACGAAATGTGA 1662
Db 6164 AATAATACCTGGATCAGATGAGAGCCCACTACGAAATGTGA 6205
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RESULT 6

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US-10-377-718-3
; Sequence 3, Application US/10377718
; Publication No. US20030175291A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuang
; TITLE OF INVENTION: MULTIPLE AND MULTIVALENT DNA VACCINES IN OVO
; FILE REFERENCE: 39734-186920
; CURRENT APPLICATION NUMBER: US/10/377,718
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 15186
; ORGANISM: Newcastle disease virus (NDV)
US-10-377-718-3
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Query Match 85.0%; Score 1412.4; DB 14; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 1 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTCGGGTTCGGG 60
Db 4544 ATGGGCTCCAGATCTTCTACAGGATCCAGTACCTCTGATGCTGACCGTTCGGGTTCGGG 4603
QY 61 CTGGCACTGAGTTGCGTCTGTCCGCAAGCTCCCTTGTATGGCAGGCTCTTGCAGTGA 120
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QY 241 TTGGAGGGGTCAACAGGACATTTGACTATTTTGTCTACCCCGCTTGGTGAATCTTATCGT 300
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Qy 361 ATTATCGCGGTGCAGCTCTCGGGTTGCCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
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Qy 4904 ATTATCGCGGTGCAGCTCTCGGGTTGCCAACCGCTGCACAGATAACAGCAGCTTCGGCT 4963
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Qy 421 CTGATACAAGCCAAACCAAAATGCTCGCCAAACATCTCTCGGGCTTAAAGAGAGAAATTCGTGCA 480
Db |||||
Qy 4964 CTGATACAAGCCAAACCAAAATGCTCGCCAAACATCTCTCGGGCTTAAAGAGAGAAATTCGTGCA 5023
Db |||||
Qy 481 ACCAATGAGGCTGTGCACGAGGTCACTGATGGATATCAAACTAGCAGTGGCAGTTGGG 540
Db |||||
Qy 5024 ACCAATGAGGCTGTGCACGAGGTCACTGATGGATATCAAACTAGCAGTGGCAGTTGGG 5083
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Qy 541 AAGATGACAGCAATTTGTTAATGACAGTTTAAATAAAGAGCTCAAGGATTCGAGTGTATTA 600
Db |||||
Qy 5084 AAGATGACAGCAATTTGTTAATGACCAATTTAATAAAGAGCTCAAGGATTCGAGTGTATTA 5143
Db |||||
Qy 601 AAAATTAACCCAGCAGGTTGGTGTAGAACTCAACCTGTATCTAATGAATTCAGTACAGTA 660
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Qy 5144 AAAATTCACAGCAAGTTGGTGTAGAGCTCAACCTGTACCTTAACCGAATTCAGTACAGTA 5203
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Qy 661 TTGGGGCCAAATCACTTCCCTGCCCTTAACCCAGCTGACTATCCAGGGCTTTTCAAT 720
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Qy 5204 TTGGGGCCAAATCACTTCCCTGCCCTTTAAACCAAGCTGACTATTCAGGCACTTTCAAT 5263
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Qy 721 CTAGCTGGTGGGAATATGGATTACTGTGTGACTAAGTTAGGTAGGGAACAACCAACTC 780
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Qy 5264 CTAGCTGGTGGGAATATGGATTACTTTAATGACTAAGTTAGGTAGGGAACAATCAACTC 5323
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Qy 781 AGCTCAATTAATGGTAGCGGCTGATCACCGGCAACCCCTATTCTGTACGACTCACAGACT 840
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Qy 5324 AGCTCAATTAATGGTAGCGGCTTAATCACCGGTAACCCCTATTCTATACGACTCACAGACT 5383
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Qy 901 ACCTACTTGGAAACCTTGTCTGTAAGTACAAACAAAGATTTGCTCAGCACTCGTCCCA 960
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Qy 5444 ACCTACTTGGAAACCTTATCGTHAGCAACACAGGGGATTTGCTCGGCACCTTGTCCCC 5503
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Qy 961 AAGTGGTGTATGAGGTGCGTTCGGTGTGATGAAGAACTTGACACCTCATACTGTATAGAG 1020
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Qy 1021 ACCGATTTGATCTATATTGTACAGAAATAGTGACATTCCTATGCTCTCTGGTATTAT 1080
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Qy 5564 ACTGACTTAGATTATATTGTACAGAAATAGTAACTGCTTCCCTATGTCCTCGTGTATTAT 5623
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Qy 1081 TCCTGTTTGAAGCGGCAATACATCGGCTTGATGTACTCGAAGACTGAAGCGGCACTCACT 1140
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Qy 5624 TCCTGTTTGAAGCGGCAATACATCGGCTTGATGTACTCGAAGACTGAAGCGGCACTTACT 5683
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Qy 1141 ACGCGGTATCATGACTCTCAAAGGCTCAGTTATTGCCAACTGTAAAGATGACAACTGAGA 1200
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Qy 5684 ACACCATACATGACTCAAAGGTTCACTCATGCCAACTGCAAGATGACAACTGAGA 5743
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Qy 1201 TGTGACAGACCCCGGGTATCATATCGCAAAATATGAGAGAGCTGTCTCTAAATAGAT 1260
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Qy 5744 TGTGTAACCCCGGGGTATCATATCGCAAACTATGAGAGAGCGGTGTCTCTAAATAGAT 5803
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Qy 1261 AGGCAATCATGCAATGCTCTATCCTTAGACGGAATTAATTTGAGGCTCAGTGGGGAATTT 1320
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Qy 5804 AACAATCATGCAATGTTTATCCTTAGCGGGGTAATCTTAAGGCTCAGTGGGGAATTC 5863
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Qy 5864 GATGCAACTTATCAGAAGAAATATCTCAATACAAGATTCTCAAGTAATTAATAACAGGCAAT 5923
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Db 5984 TTAGAGGAAAGCAACAGAAAACTAGACAAAAGTCAATGTCAAACTGACTAGCACATCTGCT 6043
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Db 1501 CTCAATCACCTATATCGTTTAACTGTATATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
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Db 6164 AATAATACCTCTAGATCAGATGAGAGCCACTACAAAAATGTGA 6205
Qy |||||

RESULT 7
US-10-429-735-3
; Sequence 3, Application US/10429735
; Publication No. US20030207836A1
; GENERAL INFORMATION:
; APPLICANT: KUO, Tsun Yuan
; TITLE OF INVENTION: VACCINE ACCELERATOR FACTOR (VAF) FOR IMPROVEMENT OF VACCINATIONS
; FILE REFERENCE: 39734-188449
; CURRENT APPLICATION NUMBER: US/10/429, 735
; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15186
; TYPE: DNA
; ORGANISM: Newcastle disease virus (NDV)
US-10-429-735-3

Query Match 85.0%; Score 1412.4; DB 15; Length 15186;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1506; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 1 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACTCTGATGCTGACCGTCCGGTCCGG 60
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Qy 4544 ATGGGCTCCAGATCTTCTACAGGATCCCAAGTACTCTGATGCTGACCTATGATGCTATCCGGTTGG 4603
Db |||||
Qy 61 CTGGCACTGATGTCGGTCTCTCCGACAAAGTCCCTTGATGCGCAGGCTCTTTCAGCTGCA 120
Db |||||
Qy 4604 CTGGTACTGATGTCGATCTCTCCGCAAACTCCATTTGATGCGCAGGCTCTTTCAGCTGCA 4663
Db |||||
Qy 121 GGGATTGTGTGACAGGACAAAGCAGTCAACATATACACCTCATCTCAGACAGGTC 180
Db |||||
Qy 4664 GGAATTGTGTGACAGGACAAAGCAGTCAACATATACACCTCATCTCCAGACAGGATCA 4723
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Qy 181 ATCATGATCAAGTACTCTCCCAAAATATGCCCAAGATAAGAGGCGTGTGCAAAAGCCCCG 240
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Qy 4724 ATCATGATCAAGTACTCTCCCAAGATAAGAGGCGTGTGCAAAAGCCCCG 4783
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Qy 4784 TTGGATGTCATACAAAGGACATTCATCTTTGCTACCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 4843
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Qy 301 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTATAGGCGCC 360
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Qy 4844 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGAGCGCTTATAGGCGCC 4903
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Qy 361 ATTATCGGGGTGACGCTCTCGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCT 420
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Qy 4904 ATTATCGGGGTGCTGCTCTTGGGTTGCACTGCGCACAATACAGCGGCGCAGCT 4963
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Qy 421 CTGATACAGGCAACCAAAATGCTGCCAACTCTCCGGCTTAAAGAGAGAAATTCGTGCA 480
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Qy 4964 CTGATACAGGCAACCAAAATGCTGCCAACTCTCCGGCTTAAAGAGAGCAATTCGCGCA 5023
Db |||||
Qy 481 ACCAATGAGGCTGTGCACGAGGTCACTGATGGAATATCAACTAGCAGTGGGAGTTGG 540
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QY 301 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGGACGCTTATAGGGCC 360
Db 1527 AGGATACAGAGTCTGTGACTACATCTGGAGGAGGGAACAGGGACGCTTATAGGGCC 1586
QY 361 ATTATCGCGGCTGAGCTCTCGGGGTTCACACCGCTGCACAGATACAGCAGCTTCGGCT 420
Db 1587 ATTATCGCGGCTGAGCTCTCGGGGTTCACACCGCTGCACAGATACAGCAGCTTCGGCT 1646
QY 421 CTGATACAGCCAAACCAAAATGTGCAACATCTCCGGCTTAAAGAGAGAATTCGTGCA 480
Db 1647 CTGATACAGCCAAACCAAAATGTGCAACATCTCCGGCTTAAAGAGAGACATTCGCCGA 1706
QY 481 ACCAATGAGCTGTGCAGAGGTCACTGATGATATATCAAACTAGCAGTGGCAGTTGGG 540
Db 1707 ACCAATGAGCTGTGCAGAGGTCACTGATGATATATCAAACTAGCAGTGGCAGTTGGG 1766
QY 541 AAGATGACGAAATTTGTTAATGACAGTTTAAATAAAGCTCAGAGAAATGGAGCTGATA 600
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QY 601 AAAATACCGCAGGTTGGTGTAGAACTCAACCTGTATCTAATGAAATGACTACAGTA 660
Db 1827 AAAATACCGCAGGTTGGTGTAGAGCTCAACCTGTATCTAATGAAATGACTACAGTA 1886
QY 661 TTGGGGCCAAATCACTTCCCTGCTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 720
Db 1887 TTGGGGCCAAATCACTTCCCTGCTTAACCCAGCTGACTATCCAGGCGCTTTACAAT 1946
QY 721 CTAGCTGGTGGGAATATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACCAACTC 780
Db 1947 CTAGCTGGTGGGAATATGGAATTAATTTGACTAAGTTAGGTGTAGGGAACCAACTC 2006
QY 781 AGCTCATTATGTTAGCGGCTGATCAGCGGAACCCCTATTCGTGAGACTACAGACT 840
Db 2007 AGCTCATTATGTTAGCGGCTGATCAGCGGAACCCCTATTCGTGAGACTACAGACT 2066
QY 841 CAGCTTTGGGTATACAGGTAAACCTACCTCAGTCGGGAACCTGAATAATATGCGTGC 900
Db 2067 CAGCTTTGGGTATACAGGTAAACCTACCTCAGTCGGGAACCTGAATAATATGCGTGC 2126
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Db 2127 ACCTACTTGGAACTTGTCTGTAAGTACAAACCAAGGATTTGCTCAGCACTCGTCCCA 2186
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Db 2187 AAGTGTGTATGAAGTTCGGTTCGTGATAGAAACTTGACACTCATCTGATATAGAA 2246
QY 1021 ACCGATTTGGATCTATATTGTACAGAAATAGTGACATTCCTATGTCCTCGGTATTAT 1080
Db 2247 ACTGACTTAGATTTATATTGTACAGAAATAGTGACATTCCTATGTCCTCGGTATTAT 2306
QY 1081 TCCTGTTTGGGGCAATACATCGGCTTGCATGCTACTCGAAGACTGAAGCGCACTCACT 1140
Db 2307 TCCTGTTTGGGGCAATACATCGGCTTGCATGCTACTCGAAGACTGAAGCGCACTCACT 2366
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Db 2367 ACACCATATATGACTATCAAGGCTCAGTATCGTATCTAATGATGACAAATGAGA 1246
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QY 1261 AGGCAATCATGCAATGTCCTATCTTAGACGGAATAACTTTAGGCTCAGTGGGGAATTT 1320
Db 2487 AAACAATCATGCAATGTCCTATCTTAGCGGGATTAATTTAGGCTCAGTGGGGAATTC 2546
QY 1321 GATGCAATCTTATCAAAAGATATCTCAATACAGATTTCTCAAGTAATGTGACAGGCAAT 1380
Db 2547 GATGTAATCTTATCAGAAGATATCTCAATACAGATTTCTCAAGTAATGTGACAGGCAAT 2606
QY 1381 CTCGATATCTCGACTGAGCTTGGGAATGTCAACAACTCGATAGTAAATGCTTTAGATAAG 1440
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Db 2607 CTTGATATCTCAACTGAGCTTGGGAATGTCAACAACTCGATAGTAATGCTTGAATAAG 2666
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QY 1561 CTAGCATGCTACCTGTGTACAGCAAAAGCGCCACAGAGACCTTGTATGCTTGGG 1620
Db 2787 CTAGCATGCTACCTGTGTACAGCAAAAGCGCCACAGAGACCTTGTATGCTTGGG 2846
QY 1621 AATAATACCTCGATCAGATGAGAGCCACTACGAAATGTGA 1662
Db 2847 AATAATACCTCGATCAGATGAGAGCCACTACGAAATGTGA 2888

RESULT 9
US-09-733-692A-60
; Sequence 60, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVS) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; FILE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 15492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pFLC.PIV32, 15492 bp in sense orientation
US-09-733-692A-60

Query Match 9.8%; Score 162.2; DB 9; Length 15492;
Best Local Similarity 46.4%; Pred. No. 4.9e-40;
Matches 634; Conservative 0; Mismatches 723; Indels 8; Gaps 3;

QY 92 CCCTTGATGCGAGGCTCTTGAGCTGCGAGGATTTGGTGACAGAGAGCAAGACGATCA 151
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QY 152 ACATATACACTCTCATCTCAGACAGGGTCAATCATAGTCAAGTTACTCCCAATATGCCCA 211
Db 5199 TGTAATACATGATGTTGGGCTAGCTTTATTTGTTGTAAATTTACTACCAATCTTCCCC 5258
QY 212 AAGATAAAGAGGCGTGTGCAAAAGCCCGTTGGAGGCGTACAAAGAGACATTCAGTACTT 271
Db 5259 CAAGCAATGGAACATGCAACATCACCAGTCTAGATGCATATATGTTACCTATTTAAGT 5318
QY 272 TGCTACCCCTTGTGTTGATTTCTTTCGTAGGATACAGAGTCTGTGACTACATCTGGAG 331
Db 5319 TGCTAACCCCTTGTGTTGATTTCTTTCGTAGGATACAGAGTCTGTGACTACATCTGGAG 5372
QY 332 GAGGGAACAGGAGGCGCTTATAGGCGCAATTTATCGGCGTGTGAGCTCTCGGGTTGCA 391
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QY 392 CCGCTGCACATACACAGCAGCTTCGGCTCTGATACAGCCCAACCAAAATGCTGCCACA 451
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Db 6092 GAGGTTTCCCGATCCCTGAATCACAATATCAATGCTTAAAGGGGAAATCTTAATTTCTTGC 6151
QY 1111 ATGTACTGGAAGACTGAAGGGCACTCACTACGCGGTACATGACTCTCAAAAGGCTTCAGTT 1170
Db 6152 ACTTTTACCCCTATTATCGGGAACCTTCTCAAGCATTTGCAATTTGCCAATGGTGTGCTC 6211
QY 1171 ATTGCAACTGTAAAGATGACAACTAGTAGATGTCAGACACCCCGGGGTATCATATCGCAA 1230
Db 6212 TATGCAACTGCAAAATCTTTGCTATGTAAGTGTGCGGACCCCTCCCATGTTGTGCTCAA 6271
QY 1231 AATTATGAGAGCTGTGTCTCTAATAGATAGGCAATCATGCAATGCTCTATCTCTTAGAC 1290
Db 6272 GATGACAAACAAAGGATCAGCAATATGATATTAAGAGGTGCTCTGAGATGATGCTTGAC 6331
QY 1291 GGAATTAATTTGAGGCTCAGTGGGAAATTTGATGCAACTTATCAAAAGAAATATCTCAATA 1350
Db 6332 ACTTTTTCATTTAGGATCACATCTACATCAATGCTACATAGCTGACAGACTTCTCAATG 6391
QY 1351 CAGAAATCTCAAGTAAATGTCAGACAGCAATCTCGATATCTCGACTGAGCTGGGAATGTC 1410
Db 6392 ATTAATGCAAAATTTTGTACATCTAAGTCTCTAGACTTTGTCAAAATCAAAATCAATTA 6451
QY 1411 AACCAACTCGATAAGTAATGCTTTAGATAAGTTAGAGGAAAGCAAC 1455
Db 6452 AACAAATCTCTTAAAGTCTGAGGATTTGGATTGAGATAGCAAC 6496
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```
RESULT 10
US-09-733-692A-62
; Sequence 62, Application US/09733692A
; Patent No. US20020155581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVS) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 15492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of
; OTHER INFORMATION: pPLC.PIV32CT, 15474 bp in sense orientation
US-09-733-692A-62
```

```
Query Match          9.8%; Score 162.2; DB 9; Length 15492;
Best Local Similarity 46.4%; Pred No. 4.9e-40;
Matches 634; Conservative 0; Mismatches 723; Indels 8; Gaps 3;

QY 92 CCCTTGATGGCAGGCTCTTGCACTGCGAGGATTTGGTGCACAGGACAAAGCAGTCA 151
Db 5139 CCAITGCTGGAGATCAACTCTCAATGATAGGGTCAATCAATCAAGATAGATCACTCA 5198
QY 152 ACATATACACCTCATCTCAGACAGGTCAATCATAGTCAAGTACTCCCAATATGCCCA 211
Db 5199 TGTACTACACTGATGGTGGCGCTAGCTTTATTTGTTGTAATTAATCTACCCATCTCCC 5258
QY 212 AAGATAAAGAGCGGTGTGCAAAAGCCCGTTGGAGCGGTACAAACAGGACATTTGACTCT 271
Db 5259 CAGCAATGGAACTGCAACATCACCAGTCTAGATGCATATAATGTTACCTTATTAAGT 5318
QY 272 TGCTCACCCCTTTGGTGAATTCATTTGCTAGGATACAAAGAGTCTGTGACTACATCTGGAG 331
Db 5319 TGCTAACACCCCTGATTTGAGAACCTGAGCAAAATTT-----TCTGCTGTACAGATACCA 5372
QY 332 GAGGGAACACAGGAGCGCTTATAGCGCCATTATCGCGGTGTCAGCTCTCGGGGTGCA 391
Db 5373 AACCCCGCGAAGACGATTTCCAGAGTCTGTTATTTGGGCTTGTCTGCTAGGATGCTA 5432
QY 392 CCGCTGCACAGATAACAGCAGCTTCGGCTCTGATACAAAGCCCAACCAAAATGTCGCCACA 451
Db 5433 CAGCTGCACAAATAACCCGAGCTGTAGCAATAGTAAAGCCCAATGCAATGCTGTGCGA 5492
QY 452 TCCTCCGGCTTAAAGAGAGAATTTGCTGCAACCAATGAGGCTGTGCAAGAGGTCACTGATG 511
Db 5493 TAAACAATCTTGCATCTTCAATTTCAATCCACCAACAGGAGATTCAGATGTGTAACCTG 5552
QY 512 GATTATCACACTAGCAGTGGAGTGGGAAGATGCAAGCAATTTGTTAATGACCAAGTTTA 571
Db 5553 CATCAAGAACTTGAACCCGAGTTCAAGCGATTTCAAGGATTCAGATCAATCAATGAGCAATG 5612
QY 572 ATAAAAACAGCTCAGGAATTTGGAATTTGAAATTTTACCCAGCAGGTTCGGTGTGAGAACTCA 631
Db 5613 TCAACGGGATACATCTGCATCATCTGCGTCCCATGATGCACTAAATGGGTCAATATTA 5672
QY 632 ACCTGTATCTAACTGAATTTGACTACAGTATTTGGGCCCAAAATCACTTCCCTGCTCTAA 691
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Db 5969 AAATTACAGAGTAGTTGTACAAAGTTCCTAATAGAAATTCAGAAATAGCAATGAACCTA 6028
QY 991 GAAGAACTTGACACTTACTATCTATATAGAGACCGAATTTGGATCTATATTTGTAAGAAATA 1050
Db 6029 CAAAACACTCCAGGCAATGATTTGTTGTCGACACCAAACTCTGTATTTTGTAGATACAAAT 6088
QY 1051 GTGACATTCCTATGTCCTGGTATTTATTCCTGTTTGGAGGCAATACATCGGCTTGC 1110
Db 6089 GAGGTTTCCCGATCCCTGGAATCACAATATCAATCTTAAAGGGGAATCTTAAATCTTTC 6148
QY 1111 ATGTACTCGAAGACTGAAGGCGCACTCACTAGCGCGTATACATGACTCTCAAAGGCTCAGTT 1170
Db 6149 ACTTTTACCCCTATTTATCGGGAACCTTCTCAAGCGATTCGCAATTTGGCAATGGTGTGC 6208
QY 1171 ATTGCCAACTGTAAGATGACAAACATGTATGATGTGACAGCCCGGGTATCATATCGCAA 1230
Db 6209 TATGCCAACTGCAATCTTTGCTATGTAGTGTGCGGACCCCTCCCATGTTGTGTCTCAA 6268
QY 1231 AATTATGGAGAGCTGTCTCTTAATAGATAGGCAATCATGCAATGTCTTATCCTTAGAC 1290
Db 6269 GATGACAAACCAAGGATCAGCAATATGATTAAGAGGTGCTCTGAGATGATGCTTGAC 6328
QY 1291 GGAATAACTTTGAGGCTCAGTGGGAATTTGATGCAACTTATCAAAAGAAATATCTCAATA 1350
Db 6329 ACTTTTTCATTTAGGATCACATCTACATTTCAATGCTCATACGTGACAGACTTCTCAATG 6388
QY 1351 CAAGATTCCTCAAGTAATCGTGACAGGCAATCTCGATATCTCGACTGAGCTTGGGAATGTC 1410
Db 6389 ATTAATGCAATATTTGTATCATCTAAGTCTCTAGACTTTGTCAAATCAAATCAATCAATA 6448
QY 1411 AACAACTCGAAGTAAGTCTTTAGATAAGTTAGAGGAAAGCAAC 1455
Db 6449 AACAAATCTCTTAAAGTCTGAGGATTTGGATTCAGATAGCAAC 6493

RESULT 12

US-10-670-695-35

; Sequence 35, Application US/10670695

; Publication No. US20040058316A1

; GENERAL INFORMATION:

; APPLICANT: Jensen, Wayne A.

; APPLICANT: Lappin, Michael R.

; APPLICANT: Rosen, David K.

; APPLICANT: Andrews, Janet S.

; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE

; FILE REFERENCE: DI-9-1

; CURRENT APPLICATION NUMBER: US/10/670,695

; CURRENT FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 09/521,738

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 35

; LENGTH: 1986

; TYPE: DNA

; ORGANISM: canine distemper virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1986)

US-10-670-695-35

Query Match

Best Local Similarity 5.6%; Score 92.8; DB 12; Length 1986;

Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 330 AGGAGGAAACAGGAGCGCTTTATAGCGCCCAATATCGCGGTGAGCTCTCGGGTTGC 389

Db 654 AGGTAGGACAAAGCGTTTGCAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 713

QY 390 ACCCGTGCACAGATAACAGAGCTTCGGCTCTGATACAGGCAACCAAAATGCTGCCAA 449

Db 714 TACAGCTGCACAAATCACTGCAGGAATAGCTTTTACATCAATCCAACTCAATGCTCAAGC 773
QY 450 CATCTCGGCTTAAAGAGAAATTTGCTGCAACCAATGAGGCTGTGCAGAGGTCACTGA 509
Db 774 AATCCAATCTCTTAAAGAACCCCTTTGAACAGCTCTAACAAAGCTATAGAAGAAATTAGGGA 833
QY 510 TGGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGAGCAAAATTTGTTAATGACCAGTT 569
Db 834 GGCTACCAAGAAACCGCTATTGCCGTTTCAAGGAGTCAGGACTACGTCAACACGAAC 893
QY 570 TAAATAACAGCTCAGGAATTTGAGTATATAAATAATACCAGAGGTTGGTGTAGAACT 629
Db 894 CGTCCCTGCCATGCAACATATCTCATGTGAATTTAGTTGGGAGAGATTTAGGTTAAGACT 953
QY 630 CAACCTGTATCACTGAATTTGACTACAGTATTCGGGCCACAAATCACTTCCCTGCGCTT 689
Db 954 GCTTCGGTATTTACTGAGTTTGTCTCAATATTTTGGCCGAGTTTACGTGACCCCTATTTC 1013
QY 690 AACCCAGCTGACTATCCAGGCGCTTTTACAATCTAGCTGGTGGGAATATGGAATTAATCTT 749
Db 1014 AGCCGAGATATCAATTCAGGCACTGATTTATGCTCTTGGAGGAGAAATTCATAAGATACT 1073
QY 750 GACTAAGTTAGG 761
Db 1074 TGAGAAAGTTGGG 1085

RESULT 13

US-09-951-061A-86

; Sequence 86, Application US/09951061A

; Publication No. US20030082204A1

; GENERAL INFORMATION:

; APPLICANT: Paolletti, Enzo

; APPLICANT: Tartaglia, James

; APPLICANT: Taylor, Jill

; APPLICANT: Gettig, Russell

; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)

; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE

; TITLE OF INVENTION: RECOMBINANTS

; NUMBER OF SEQUENCES: 143

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff

; STREET: 300 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/951,061A

; FILING DATE: 13-SEP-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/354,138

; FILING DATE: 15-JUL-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/224,657

; FILING DATE: 16-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/073,962

; FILING DATE: 08-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/776,867

; FILING DATE: 23-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/621,614

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,283

; FILING DATE: 31-AUG-1993

Best Local Similarity 50.9%; Pred. No. 5.4e-18;
Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 330 AGGAGGGAACAGGAGCCCTTATAGCGCCATTATCGCGGTGCGAGTCTCGGGTTGC 389
Db 1422 AGGTAGGAGACAAAGCGCTTTTGCAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 1363

QY 390 AACCGCTCACAGATAACAGCAGCTTCGGCTGTGATACAGCCCAAAATGCTGCCAA 449
Db 1362 TACAGCTGCACAAATCACTGAGGAATAGCTTTACATCAATCCAACTCAATGCTCAAGC 1303

QY 450 CATCTCCGGCTTAAAGAGAGAAATGCTGCAACCAATGAGGTGTGACGAGGTCACTGA 509
Db 1302 AATCCAATCTCTAGAACCGCTTGACAGCTCAACCAAGCTATAGAGAAATTAGGA 1243

QY 510 TGGATTATCAAACTAGCAGTGGCAGTGTGGGAGAGCAGCAATTTGTTAATGACCACT 569
Db 1242 GGTACCCCAAGAAACCGCTTCATTCGGCTTCAGGAGTCCAGGACTACGTCAACCAAGAACT 1183

QY 570 TAATAAAACAGCTCAGGAATGGAGTGTATATAAAATTAACCCAGCAGGTGTGTAGAACT 629
Db 1182 GTCCCTGCCATGCAATATGTCAATGTAATAGTGTGGCAGAGATTAGGTTAGACT 1123

QY 630 CAACCTGTATCACTGAATTAATGACTACAGTATTCGGGCCCAAAATCACTTCCCTGCGCT 689
Db 1122 GCTTCGGTATTATCTAGTGTGTCAATATTTGGCCGAGTTTACGTGACCTTATTTTC 1063

QY 690 AACCCAGCTGACTATCCAGGCGCTTACAACTAGCTGTGGGATATGGAATTAATCTGTT 749
Db 1062 AGCCGAGATATCAATTCAGGCACTGATTATGCTCTTGGAGGAGAAATTCATAAGATACT 1003

QY 750 GACTAAGTTAGG 761
Db 1002 TGGGAAGTTGG 991

RESULT 15
US-09-951-061A-93/c
; Sequence 93, Application US/09951061A
; Publication No. US20030082204A1
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; APPLICANT: Gettig, Russell
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/951,061A
; FILING DATE: 13-SEP-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/354,138
; FILING DATE: 15-JUL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,657
; FILING DATE: 16-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,962
; FILING DATE: 08-JUN-1993

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/776,867
;; FILING DATE: 23-OCT-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/621,614
;; FILING DATE: 30-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/938,283
;; FILING DATE: 31-AUG-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/621,614
;; FILING DATE: 30-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/105,483
;; FILING DATE: 12-AUG-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/847,951
;; FILING DATE: 06-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/713,967
;; FILING DATE: 11-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07,666,056
;; FILING DATE: 07-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Frommer, William S.
;; REGISTRATION NUMBER: 25,506
;; REFERENCE/DOCKET NUMBER: 454310-2860
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 840-3333
;; TELEFAX: (212) 840-0712
;; INFORMATION FOR SEQ ID NO: 93:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4604 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-09-951-061A-93

Query Match 5.6%; Score 92.8; DB 10; Length 4604;
Best Local Similarity 50.9%; Pred. No. 5.6e-18;
Matches 220; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 330 AGGAGGGAACAGGAGCCCTTATAGCGCCATTATCGCGGTGCGAGTCTCGGGTTGC 389
Db 1530 AGGTAGGAGACAAAGCGCTTTTGCAGGAGTGTACTTGCAGGTGTAGCTTTAGGAGTGC 1471

QY 390 AACCGCTGCACAGATAACAGCAGCTTCGGCTCTGTATACAGCCCAAAATGCTGCCAA 449
Db 1470 TACAGCTGCACAAATCACTGAGGAATAGCTTTACATCAATCCAACTCAATGCTCAAGC 1411

QY 450 CATCTCCGGCTTAAAGAGAGAAATGCTGCAACCAATGAGGTGTGACAGGTCACTGA 509
Db 1410 AATCCAATCTCTTAGAACCCGCTTGACAGCTCTAACAAAGCTATAGAGAAATTAGGA 1351

QY 510 TGGATTATCACACTAGCAGTGGCAGTTGGGAGAGATGAGCAATTTGTTAATGACCACT 569
Db 1350 GGCTACCCCAAGAAACCGCTCAATTCGGTTCAGGAGTTCAGGACTACGTCAACAGAACT 1291

QY 570 TAATAAAACAGCTCAGGAATGGAATGTATATAAAATTAACCCAGCAGGTGTGTAGAACT 629
Db 1290 GGTCCCTGCCATGCAACATATGTCAATGTAATAGTTAGTTGGGAGAGATTAGGTTAAGACT 1231

QY 630 CAACCTGTATCTAATGTAATGACTACAGTATTCGGGCCCAAAATCACTTCCCTGCGCT 689
Db 1230 GCTTCGGTATTATCTAGTGTGTCAATATTTGGCCCGAGTTTACGTGACCTTATTTTC 1171

QY 690 AACCCAGCTGACTATCCAGGCGCTTTTACAAATCTAGCTGGTGGGAATATGGAATTAATCTGTT 749
Db 1170 AGCCGAGATATCAATTCAGGCACTGATTATGCTCTTGGAGGAGAAATTCATAAGATACT 1111

QY 750 GACTAAGTTAGG 761

Db 1110 TGGGAAGTTGGG 1099
|||||

Search completed: April 18, 2004, 01:19:10
Job time : 698 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 3940 Seconds

(without alignments)
12596.686 Million cell updates/sec

Title: US-10-725-841-1

Perfect score: 1662

Sequence: 1 atgggctccagatcttctac.....gagccactacgaaatgtga 1662

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.8	5.3	692	12	BG661033
C 2	43.2	2.6	801	29	BX213898
C 3	41	2.5	994	13	BX414650
C 4	40.8	2.5	816	28	BH183366

C 5	40.8	2.5	816	29	CNS070JL
C 6	39	2.3	387	12	B1072343
C 7	39	2.3	463	29	CE051404
C 8	39	2.3	474	13	B0532151
C 9	39	2.3	475	13	B0529885
C 10	39	2.3	480	13	B0530741
C 11	39	2.3	507	14	CD081007
C 12	39	2.3	509	13	B0532638
C 13	39	2.3	517	13	B0529996
C 14	39	2.3	626	28	BH531701
C 15	38.8	2.3	406	10	AY032979
C 16	38.8	2.3	462	13	B0531300
C 17	38.8	2.3	463	13	B0530551
C 18	38.8	2.3	693	29	C0529583
C 19	38.4	2.3	491	28	B2267917
C 20	38.4	2.3	691	28	BH978172
C 21	38.4	2.3	936	29	CNS00144
C 22	38.2	2.3	311	10	BB237765
C 23	37.8	2.3	446	13	B0529785
C 24	37.6	2.3	885	13	BX425603
C 25	37.6	2.3	891	13	B0453464
C 26	37.6	2.3	1099	13	CC273209
C 27	37.4	2.3	694	29	CE465529
C 28	37.4	2.3	1200	13	BX387778
C 29	37.2	2.2	445	13	B0530296
C 30	37.2	2.2	446	13	B0529830
C 31	37.2	2.2	491	14	CD333801
C 32	37.2	2.2	500	12	BP190449
C 33	37.2	2.2	1146	13	BX446722
C 34	37	2.2	268	9	AU227481
C 35	37	2.2	411	28	AZ556169
C 36	37	2.2	522	28	AQ150073
C 37	36.8	2.2	860	29	CG332506
C 38	36.8	2.2	4254	11	AK083774
C 39	36.6	2.2	336	10	BB166428
C 40	36.6	2.2	571	29	CE103119
C 41	36.4	2.2	787	29	CNS010B7
C 42	36.4	2.2	1083	12	BM467292
C 43	36.2	2.2	530	12	BJ360381
C 44	36.2	2.2	1022	29	CNS03RIF
C 45	36	2.2	312	12	BJ360628

ALIGNMENTS

RESULT 1	BG661033	692 bp	mRNA	linear	EST 26-APR-2001
LOCUS	N339 SSH-HCA-U library Homo sapiens cDNA, mRNA sequence.				
DEFINITION	BG661033				
ACCESSION	BG661033				
VERSION	BG661033.1	GI:13805211			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Zhang, Z. and DuBois, R.N.				
TITLE	Detection of differentially expressed genes in human colon cancer cells treatment with NS-398 using suppression subtractive hybridization and differential screening				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Zhonghua Zhang Department of Medicine Vanderbilt Medical Center MCN C-2104, 1161 21st Ave. South, Nashville, TN 37212, USA Tel: 615 343 1369 Fax: 615 343 6229 Email: zhonghua.zhang@mcmail.vanderbilt.edu DNA sequencing by: Vanderbilt Medical Center DNA sequencing core laboratory. This is a fragment of gene that up-regulated by NS-398 treatment.				


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Query Match      2.5%; Score 41; DB 13; Length 994;
Best Local Similarity 19.7%; Pred. No. 1.4; Mismatches 3; Gaps 1;
Matches 92; Conservative 167; Indels 206;

Qy 1177 AACTGTAAGATGACAAACATGTAGATGTGCAGACCCCGGGTATCATATCGCAAAATTAT 1236
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 AAARWRDRWTAAWAAXKKWADWTITKTKKADADWDGDDWDATAWWAADDDAW 887

Qy 1237 GGAGAAGCTGTCTCTTAATAGATAGGCAATCATGCAATGTCCTATCCTTAGACGGAATA 1296
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 986 AARWAAATWTTDWT--AWTRKDKATWKADDDAKTKTTTTTTTTTKWKAATDAGWT 830

Qy 1297 ACTTTGAGGCTCAGTGGGGAATTTGATCGCACTTATCAAGAATATCTCAATACAGAT 1356
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 829 AKWADATWADAADAAARAAWRAAAWAAADADWWWWDAADAAWAAWD 770

Qy 1357 TCTCAAGTATCGTGACAGGCAATCTCGATATCTCGACTGAGCTTGGGAATGTCAACAAC 1416
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 769 TKDKRAWRADWARAAAAAAMDWGRGRADAAAGKDKARAAMWDGAGRDKDRDWAARWD 710

Qy 1417 TCGTAAGTATGCTTTAGATAGTTAGAGAAAGCAACAGCAAACTAGACAAAGTCAAT 1476
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 709 DADAARRAAAAAATATWATWTKWKDKDWAATAAATATKKGKRDARDDDWAATTTT 650

Qy 1477 GTCAAACTGACCAACATCGCTCTCATCACCTATATCTGTTTAACTGTCATATCTTT 1536
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 649 TTTTAAWADKAWKKWATTTTTTTTTTTTTTTTTTKTKTKTTAKWTWDWADDDTTTTT 590

Qy 1537 GTTTGGTATCTACTTACGCTGGTTCTAGCATGCTACCTGATGTACAAGCAAAAGCGCAA 1596
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 589 TTTTWTWAAATTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 530

Qy 1597 CAGAAGCTTTGATGGCTTGGGAATAATACCTGATGATGATGAGA 1644
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 529 RRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 482
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RESULT 4
LOCUS BH183366
DEFINITION 023_G_14-21 SmBAC1 Schistosoma mansoni genomic clone 023G14 5',
genomic survey sequence.
ACCESSION BH183366
VERSION BH183366.1 GI:16288520
KEYWORDS GSS.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE 1 (bases 1 to 816)
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni
bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
JOURNAL 20247247
MEDLINE 10783255
PUBMED Other_GSSs: 023_G_14-rev
COMMENT Contact: Pierce RJ
INSERM U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DG0AA023BD07Cp1
Plate: 023 row: G column: 14
Seq primer: M13 -21 primer
Class: BAC ends
High quality sequence stop: 816.
Location/Qualifiers
1. .816
/organism="Schistosoma mansoni"
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/mol_type="genomic DNA"
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/db_xref="taxon:6183"
/clone="023G14"
/sex="mixed"
/dev_stage="cercariae"
/lab_host="Biomphalaria glabrata"
/clone_lib="SmBAC1"
/notes="Vector: pBeloBAC 11; Site 1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."

ORIGIN

Query Match      2.5%; Score 40.8; DB 28; Length 816;
Best Local Similarity 35.4%; Pred. No. 1.4;
Matches 80; Conservative 41; Mismatches 105; Indels 0; Gaps 0;

Qy 1329 TTATCAAAAGATATCTCAATACAAAGATCTCAAGTAATCTGACAGGCAATCTCGATAT 1388
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Db 536 TTAGAGAAAANATATATATATATAAATAAATAAATAAATAAATAAATAAATAAATAA 477

Qy 1389 CTGAGTACGCTGGGAATCTCAACAACTCGAATGTAAGTAACTTTAGATAGTATAGGA 1448
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 ATATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 417

Qy 1449 AAGCAACAGCAAACTAGCAAGTCAATGTCAACTGACAGGACATCCGCTCTCATCAC 1508
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 AAAAAAAYAAAGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 357

Qy 1509 CTATATCGTTTAACTGTCATATCTCTTGTGTTGGTATATCTTAGC 1554
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 YGYBYKYTKYTGTTGTTGKTGKTGKTGTTGCBGCKKMGYAGC 311
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RESULT 5
LOCUS CNS070JL/c
DEFINITION T7 end of clone 023BD07 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni, genomic survey sequence.
ACCESSION AL620307
VERSION AL620307.1 GI:16034449
KEYWORDS GSS.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE 1 (bases 1 to 816)
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W.,
Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni
bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
JOURNAL 20247247
MEDLINE 10783255
PUBMED Other_GSSs: 1 (bases 1 to 816)
COMMENT Direct Submission
INSERM U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DG0AA023BD07Cp1
Plate: 023 row: G column: 14
Seq primer: M13 -21 primer
Class: BAC ends
High quality sequence stop: 816.
Location/Qualifiers
1. .816
/organism="Schistosoma mansoni"
/mol_type="genomic DNA"
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RESULT 8
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LOCUS
DEFINITION APEX1.1 C10 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ532151
VERSION BQ532151.1 GI:33459914
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 1 row: C column: 10
            Seq primer: M13 Rev.
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            1..474
            /organism="Saccharum officinarum"
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            /cultivar="CP72-2086"
            /db_xref="taxon:4547"
            /tissue_type="Leafroll including apex"
            /dev_stage="After floral induction"
            /clone_lib="pSLR"
            /note="Vector: UniZAP XR/pBluescript; Site_1: EcoRI;
            Site_2: XhoI"
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Best Local Similarity 50.8%; Pred. No. 3-7;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 370 GGTGACGCTCTCGGGTTGCAACCGCTGCACAGATACACAGCTTGGCTCTGATACAA 429
Db |||||
283 GGTGACGCGTTGGCGTGGATGGCGGCGAGAGGAGCAACAGTTCGCGCTCTGGTTTCA 342
QY 430 GCCAACCAAAATGCTGCCACATCTCCGCTTAAAGAGAGATTGCTGCAACCAATGAG 489
Db |||||
343 CCCACCAAGACTTCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
Db |||||
403 GGTGGACGAGATCCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 550 CAA 552
Db |||||
463 CAA 465

RESULT 9
BQ529885
LOCUS
DEFINITION APEX1.3 E11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ529885
VERSION BQ529885.1 GI:33457648
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 1 row: C column: 10
            Seq primer: M13 Rev.
FEATURES
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            /tissue_type="Leafroll including apex"
            /dev_stage="After floral induction"
            /clone_lib="pSLR"
            /note="Vector: UniZAP XR/pBluescript; Site_1: EcoRI;
            Site_2: XhoI"
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Best Local Similarity 50.8%; Pred. No. 3-7;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 370 GGTGACGCTCTCGGGTTGCAACCGCTGCACAGATACACAGCTTGGCTCTGATACAA 429
Db |||||
283 GGTGACGCGTTGGCGTGGATGGCGGCGAGAGGAGCAACAGTTCGCGCTCTGGTTTCA 342
QY 430 GCCAACCAAAATGCTGCCACATCTCCGCTTAAAGAGAGATTGCTGCAACCAATGAG 489
Db |||||
343 CCCACCAAGACTTCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
Db |||||
403 GGTGGACGAGATCCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 550 CAA 552
Db |||||
463 CAA 465

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clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu
            Plate: 3 row: E column: 11
            Seq primer: M13 Rev.
FEATURES
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            /organism="Saccharum officinarum"
            /mol_type="mRNA"
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            /tissue_type="Leafroll including apex"
            /dev_stage="After floral induction"
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            Site_2: XhoI"
ORIGIN
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Best Local Similarity 50.8%; Pred. No. 3-7;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 370 GGTGACGCTCTCGGGTTGCAACCGCTGCACAGATACACAGCTTGGCTCTGATACAA 429
Db |||||
283 GGTGACGCGTTGGCGTGGATGGCGGCGAGAGGAGCAACAGTTCGCGCTCTGGTTTCA 342
QY 430 GCCAACCAAAATGCTGCCACATCTCCGCTTAAAGAGAGATTGCTGCAACCAATGAG 489
Db |||||
343 CCCACCAAGACTTCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 490 GCTGTGCACGAGTCACTGATGATTATCAAACTAGCAGTGGCAGTTGGGAAGATGCAG 549
Db |||||
403 GGTGGACGAGATCCCATACCTACTTCCATCTCTGGAATCCCAAGCAAGCGTCTTCAT 402
QY 550 CAA 552
Db |||||
463 CAA 465

RESULT 10
BQ530741
LOCUS
DEFINITION APEX1.2 H11 pSLR Saccharum officinarum cDNA 5', mRNA linear EST 06-AUG-2003
ACCESSION BQ530741
VERSION BQ530741.1 GI:33458504
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
            Paterson,A.H.
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            111 Riverbend Rd., Athens, GA 30602, USA
            Tel: 706 583 0162
            Fax: 706 583 0160
            Email: paterson@dogwood.botany.uga.edu

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Plate: 2 row: H column: 11
Seq primer: M13 Rev.

FEATURES

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1. .480
Location/Qualifiers
/organism="Saccharum officinarum"
/mol_type="mRNA"
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/db_xref="taxon:4547"
/tissue_type="Leafroll including apex"
/dev_stage="After floral induction"
/clone_lib="pSLR"
/note="Vector: UnizAP XR/pBluescript; Site_1: EcoRI;
Site_2: XhoI"

ORIGIN

Query Match 2.3%; Score 39; DB 13; Length 480;

Best Local Similarity 50.8%; Pred. No. 3.8;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 370 GGTGAGCTCTCGGGTTCACCGCTGCACAGATAACAGCAGCTTCGGCTCTGATACAA 429
|||||
Db 283 GGTGAGCGCTTGGCGTGATGGCGCGAGAGGAGCAACAGTTCGCCCTCTGGTTGCA 342
|||||
QY 430 GCCAACCAAAATGTCGCCAATCTCTCGGGTTAAAGAGAGAATTCGTCACCAATGAG 489
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Db 343 CCCACCAAGGACTTCCATACCTACTCTCTGGAATCCCAAGCAGCTCATCTTCAT 402
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QY 490 GCTGTGACAGGTCACGTGATGATATACAACTAGCAGTGGCGATGGGAAGATGAG 549
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Db 403 GGTGACAGAGATGCCATCAGGACTCCGGAACCTGGAGAGCAAGGGGGTGGCGTTCCC 462
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QY 550 CAA 552
|||||
Db 463 CAA 465

RESULT 11

LOCUS CD081007 507 bp mRNA linear EST 14-SEP-2003
DEFINITION MA3-9999U-M317-D07-U.G MA3-0001 Schistosoma mansoni cDNA clone
ACCESSION MA3-9999U-M317-D07.6, mRNA sequence.
VERSION CD081007.1 GI:34632000
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 507)
Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Jr.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Wenck, C.F.M.,
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acoelomate human parasite Schistosoma
mansoni
Nat. Genet. 35 (2), 148-157 (2003)
22879926
Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquímica
Instituto de Química - Universidade de São Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,
Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjovski@usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen

in the following URL <http://bioinfo.iq.usp.br/schisto/>
Plate: MA3-9999U-M317 row: 7 column: D.

FEATURES

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Location/Qualifiers
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MA3-9999U-M317-D07.G"
/sex="mixed pool"
/dev_stage="adult"
/lab_host="Mus musculus"
/clone_lib="MA3-0001"

ORIGIN

Query Match 2.3%; Score 39; DB 14; Length 507;

Best Local Similarity 48.1%; Pred. No. 3.9;
Matches 87; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1432 TTAGATAAGTTAGAGGAAGCAACAGCAATAGCAAGGTCAATGTCAAACTGACCAGC 1491
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Db 127 TGAACAGTTGCGCAATACACAGACAACACACCGTTATTAAGCGTTACTAGC 186
|||||
QY 1492 ACATCCGCTCTCATCACCTATATCTTTAACTGTCTATCTCTTTGGTATATCTT 1551
|||||
Db 187 TAAACCTGTCTCATCAGCTTTATTCCTTGAATAATTATTTCAGACATTTAATCGTCACTT 246
|||||
QY 1552 AGCCTGGTTCTAGCATGCTACTGATGTACAGCAAGGCGACAGACCTTGTTA 1611
|||||
Db 247 GGATCCAATCTTCATGTGTACGTTTACCAAGCGATNNNNNNNNNNNAGCAATAA 306
|||||
QY 1612 T 1612
|||||
Db 307 T 307

RESULT 12

LOCUS BQ532638 509 bp mRNA linear EST 06-AUG-2003
DEFINITION APEX2.7 G05 PSLR Saccharum officinarum cDNA 5', mRNA sequence.
ACCESSION BQ532638
VERSION BQ532638.1 GI:33460401
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 509)
Schulze, S.R., Ma, H.M., Meizhu Yang, J., Bowers, J.E., Mirkov, E. and
Paterson, A.H.
An EST survey of the sugarcane transcriptome
Unpublished (2002)
Contact: Paterson, A.H.
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
111 Riverbend Rd., Athens, GA 30602, USA
Tel: 706 583 0162
Fax: 706 583 0160
Email: paterson@dogwood.botany.uga.edu
Plate: 7 row: G column: 05
Seq primer: M13 Rev.
source
1. .509
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="CP72-2086"
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/tissue_type="Leafroll including apex"
/dev_stage="After floral induction"
/clone_lib="pSLR"
/note="Vector: UnizAP XR/pBluescript; Site_1: EcoRI;
Site_2: XhoI"

ORIGIN


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Query Match      2.3%; Score 39; DB 13; Length 509;
Best Local Similarity 50.8%; Pred. No. 3.9;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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Db 283 GGTGACGCGCTTGGCGTGGATGGCGGCGAGGAGCAACAGTTCCGGCTCTGGTTGGA 342

QY 430 GCCAACCAAAATGCTGCAACATCTCCGGTTTAAAGAGAGAATGTGCAACCAATGAG 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 CCCACCAAGGACTTCATACCTACTCTGGAATCCCAAGCAGCGTCATCTTCAT 402

QY 490 GCTGTGCACGAGGTCAGTGATGATTATCACACTAGCAGTGGCAGTTGGAGATCGAG 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 GGTGGACGAGATGCCCATCAGGACTTCCGGAACCTGGAGAGCAAGGGGTGGCGTTCCC 462

QY 550 CAA 552
    |||
Db 463 CAA 465

RESULT 13
LOCUS BQ529996 517 bp mRNA linear EST 06-AUG-2003
DEFINITION APEX1 3 E01 pSLR Saccharum officinarum cDNA 5', mRNA sequence.
ACCESSION BQ529996
VERSION BQ529996.1 GI:33457759
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 517)
AUTHORS Schulze,S.R., Ma,H.M., Meizhu Yang,J., Bowers,J.E., Mirkov,E. and
TITLE An EST survey of the sugarcane transcriptome
JOURNAL Unpublished (2002)
COMMENT Contact: Paterson, A.H.
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
111 Riverbend Rd., Athens, GA 30602, USA
Tel: 706 583 0162
Fax: 706 583 0160
Email: paterson@dogwood.botany.uga.edu
Plate: 3 row: E column: 01
Seq primer: M13 Rev.
FEATURES
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Location/Qualifiers
1..517
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/dev_stage="After floral induction"
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Site_2: XhoI"

Query Match      2.3%; Score 39; DB 13; Length 517;
Best Local Similarity 50.8%; Pred. No. 3.9;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 370 GGTGACGCTCTCGGGTTGCAACCGCTGCACAGATAACAGCAGCTTCGGCTCTGATACAA 429
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Db 283 GGTGACGCGCTTGGCGTGGATGGCGGCGAGGAGCAACAGTTCCGGCTCTGGTTGGA 342

QY 430 GCCAACCAAAATGCTGCCACATCTCCGGCTTAAAGAGAGAATGTGCAACCAATGAG 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 490 GCTGTGCACGAGTCACTGATGATTATCACACTAGCAGTGGCAGTTGGAGATCGAG 549
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Db 403 GGTGGACGAGATGCCCATCAGGACTTCCGGAACCTGGAGAGCAAGGGGTGGCGTTCCC 462

QY 550 CAA 552
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Db 463 CAA 465

RESULT 14
LOCUS BH531701 826 bp DNA linear GSS 14-DEC-2001
DEFINITION BOHGP20TF BOHG Brassica oleracea genomic clone BOHGP20, genomic
survey sequence.
ACCESSION BH531701
VERSION BH531701.1 GI:17752135
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 826)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOHGP20TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
source
Location/Qualifiers
1..826
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHGP20"
/clone_lib="BOHG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
Query Match      2.3%; Score 39; DB 28; Length 826;
Best Local Similarity 46.5%; Pred. No. 5.3;
Matches 126; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 509 ATGGATTATCAACAATAGCAGTGGCAGTTGGGAAGATGCAGCAATTTGTTAATGACCAGT 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ATTAATTATGACAAATATAGGATCATAGTATTAATAATACAAATTTTGAAGTTAAATT 210

QY 569 TTAATAAAACAGCTCAGGAATTGGACTGTATAAAAATTACCCAGCAGGTTGGTGTAGAAC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 TGAAGTTGTATTTTGTAGAAAATGACATCTTGAAATTTCAAAATATAGAAATTTTACAAAAA 270

QY 629 TCAACCTGTATCTAAGTGAATGACTACAGTATTCGGGCCACAAATCACTTCCCTGCGCT 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 AAAAATTTTGAATAATCCCTATCGGCTGATCCCGTCCGGGAGGAACGCACCTTAGTG 330

QY 689 TAACCCAGCTGACTATCCAGGCGCTTTACAATCTAGCTGGTGGGAATATGGATTACTTCT 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 CTACAAAGTGGACTATCCGAAAAACGTACCACTGCTCCCTGACCGAGTTTGGAAATACCTTC 390

QY 749 TGACTAAGTTAGTGTAGGGAACAAACCAACT 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 CGACTAATGTTAGGGGTGGACCAATCATCT 421

```

Search completed: April 18, 2004, 02:29:38
Job time : 3953 secs

Search completed: April 18, 2004, 02:29:38
Job time : 3953 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSSTRIPVPLMLTVRVA.....KTLWLGNNTLDQMRAATKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2724	98.8	553	2 AAR10065	Aar10065 Newcastle
2	2716	98.5	553	6 ABR56236	Abr56236 Newcastle
3	2620	95.0	1103	6 ABR39678	Abr39678 Amino aci
4	2616	94.9	553	3 AAY51231	Aay51231 Newcastle
5	2610	94.7	553	2 AAR58858	Aar58858 Newcastle
6	2610	94.7	553	2 AAR49141	Aar49141 Newcastle
7	2610	94.7	553	2 AAW06828	Aaw06828 Newcastle
8	2610	94.7	553	2 AAW10691	Aaw10691 Newcastle
9	2610	94.7	553	3 AAY21983	Aay21983 Seq ID No
10	2610	94.7	553	3 AAY58183	Aay58183 NDV fusio
11	2610	94.7	553	3 AAB36039	Aab36039 Protein e
12	2606	94.5	553	2 AAR14480	Aar14480 Newcastle
13	2606	94.5	553	2 AAW44941	Aaw44941 Newcastle
14	2603	94.4	553	1 AAP70176	Aap70176 Sequence
15	2493.5	90.4	564	5 ABG31709	Abg31709 Newcastle
16	2401	87.1	526	1 AAP80986	Aap80986 Sequence
17	2386	86.5	526	2 AAR20501	Aar20501 Newcastle
18	2086.5	75.7	436	6 ABO10250	Abo10250 Newcastle
19	2085	74.9	437	6 AAU14030	Aau14030 Peptide s
20	717	26.0	529	6 ABJ18515	Abj18515 Human Cry
21	715	25.9	529	6 ABJ18516	Abj18516 Canine pa
22	714	25.9	551	6 ABJ18506	Abj18506 Human Cry
23	712	25.8	551	6 ABJ18514	Abj18514 Simian vi
24	707	25.6	551	6 ABJ18513	Abj18513 Simian vi
25	706	25.6	529	4 ABP98712	Abp98712 Canine pa

ALIGNMENTS

RESULT 1

AAR10065

ID AAR10065 standard; protein; 553 AA.

XX AAR10065;

XX AC

XX XX

DT 25-MAR-2003 (revised)

DT 14-MAR-1991 (first entry)

XX XX

DE Newcastle disease virus (NDV) F gene product.

XX XX

KW Avipoxvirus; fowlpoxvirus; vaccine.

XX XX

OS Newcastle disease virus.

XX XX

PN EP404576-A.

XX XX

PD 27-DEC-1990.

XX XX

PF 21-JUN-1990; 90EP-00306806.

XX XX

PR 22-JUN-1989; 89JP-00160157.

XX XX

PA (JAPG) NIPPON ZEON KK.

PA (SHIO) SHIONOGI & CO LTD.

XX (YANA/) YANAGIDA N.

PI Yangida N, Saeki S, Okawa S, Knamogawa K, Iritani Y, Sawaguchi K;

XX WPI: 1991-001591/01.

DR N-PSDB; AAR10060.

XX XX

PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus in region non-essential for proliferation, used as live vaccine in fowls.

XX XX

PS Claim 3; Fig 3; 23pp; English.

XX XX

CC The sequence encoding the protein may be incorporated into a recombinant

CC Avipoxvirus and used as a live vaccine in fowls, providing immunity to

XX fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)

XX XX

SQ Sequence 553 AA;

XX XX

Query Match 98.8%; Score 2724; DB 2; Length 553;

Best Local Similarity 98.4%; Pred. No. 9.8e-226;

Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVCTSSLDRPLAAGIVTGDKAVNIYTSQTGS 60

Abj18507 Human Cry
Aab67476 Amino aci
Aar24076 Para-infl
Aar83304 Canine di
Aam47653 Canine di
Aab08102 Amino aci
Aam50124 Canine di
Aab73722 Measles v
Aar42394 Moraten h
Aar34540 F protein
Aar42396 Chicago 1
Aar42397 Consensus
Aar42395 San Diego
Aar94759 Mutant me
Aab73721 Measles v
Aaw94760 Mutant me
Abj18509 Human Cry
Aar3283 Parainflu
Abo10249 Canine di
Aaul4029 Peptide s

26 696.5 25.3 532 6 ABJ18507
27 694.5 25.2 538 4 AAB67476
28 689 25.0 542 2 AAR24076
29 623.5 22.6 662 2 AAR83304
30 623.5 22.6 662 5 AAM47653
31 621.5 22.5 662 3 AAB08102
32 621.5 22.5 662 4 AAM50124
33 610.5 22.1 550 2 AAR42394
34 610.5 22.1 550 4 AAB73722
35 608.5 22.1 550 2 AAR34540
36 606.5 22.0 550 2 AAR42396
37 606.5 22.0 550 2 AAR42397
38 606.5 22.0 550 2 AAR42395
39 605.5 22.0 550 2 AAW94759
40 605.5 22.0 550 4 AAB73721
41 602.5 21.9 550 2 AAW94760
42 590.5 21.4 449 6 ABJ18509
43 552 20.0 539 2 AAR3283
44 534 19.4 438 6 ABO10249
45 522.5 19.0 439 4 AAU14029

1	MGSRSTRIPVPLMLTVRIMLALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQRTGS	60
61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
61	IIIKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
121	IIGGAALGVATAAQITTAASALIQANQNAANTILRLKERIAATNEAVHEVTDGLSQLAVAG	180
121	IIGVALGVATAAQITTAASALIQANQNAANTILRLKESIAATNEAVHEVTDGLSQLAVAG	180
181	KMQQFVNDQFNKTAQELDCIKITQOVGVYELNLYLTETLTVFGPQITSPALQTTLTQALYN	240
181	KMQQFVNDQFNKTAQELDCIKITQOVGVYELNLYLTETLTVFGPQITSPALQTTLTQALYN	240
241	LAGGNMDDLTKLGVGNNOQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
241	LAGGNMDDLTKLGVGNNOQLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
301	TYLETLSVSTTKGFASALVPKVVWKGVSIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
301	TYLETLSVSTTKGFASALVPKVVWKGVSIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
361	SLCSGNTSACMYSKTEGALTTPYMTLKGSVIANCRWTTCCRADPPGIIISQNYGEAVSLID	420
361	SLCSGNTSACMYSKTEGALTTPYMTLKGSVIANCRWTTCCRADPPGIIISQNYGEAVSLID	420
421	RQSCNVLSLDGITLRLSGEFDAYQKNISIQDSQVIVTGNLIDISTELGNVNNISISNALDK	480
421	RQSCNVLSLDGITLRLSGEFDAYQKNISIQDSQVIVTGNLIDISTELGNVNNISISNALDK	480
481	LEENSKLDKVNVKLTSTSALITYITVLTVISLVCGLISLVLACYLWYKQAKQKTLMLWG	540
481	LEENSKLDKVNVKLTSTSALITYITVLTVISLVCGLISLVLACYLWYKQAKQKTLMLWG	540
541	NNTLDMQBRATTQNN	553
541	NNTLDMQBRATTQNN	553

RESULT 2
ABR56236
ID ABR56236 standard: protein: 553 AA.

AC ABR56236;

20-NOV-2003 (first entry)

Newcastle disease virus (NDV)

F-protein; virucide; vaccine; anti-viral; Fusion

PROTEIN CO-ORDINATE DATA.

09 Newcastle disease virus.

PM WO2003040178-A1.

15-MAY-2003.

08-NOV-2002: 2002WO-AU001522.

09-NOV-2001: 2001AU-00008784.

(BIOT-) BIOTA HOLDINGS LTD.

XX
PF
Morton C.T. Parker MW.
Ryan J.

WDI: 2003-111531/11

xx Identifying, screening or modifying anti-viral agents, by generating a 3-
pt dimensional structure model of respiratory syncytial virus-F protein
pt having a target site to interact with an anti-viral agent that inhibit
pt RSV-F.
pt

XX
PS
XX
Disclosure; Fig 1; 224pp; English.
XX
The present invention relates to a method (M1) for identifying a
CC
candidate anti-viral agent (I), screening compounds and/or chemical
CC
complexes for (I), modifying (I) to improve anti-viral activity, or
CC
producing anti-viral agents, by generating a 3-dimensional structure
CC
model of Respiratory Syncytial Virus (RSV) Fusion (F)-protein with 3-
CC
dimensional structure of target site to which an anti-viral agent may
CC
interact and thus inhibit RSV-F protein activity. The present sequence is
CC
the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment
CC
with the RSV F-protein sequence (ABR56234)

Sequence 553 AA;

Query Match 98.5%; Score 2716; DB 6; Length 553;

BEST LOCAL SIMILARITY 98.2%; FREQ. NO. 4.00 1257
Matches 543; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

1 MGSRSSTRTPVPLMLTVRVALALSCVCPSTSSLDGRPLAAAGIVTGDKAVNIYTSSQTGS 60

1 MCSRSSSTRI PVPI.MI.TTVRVMIALSCVCPTSDGRPLAAGIVVTGDKAVNIYTSSQTGS 60

0-61 IIVKII.PNMPKDKEACAKAPI.EAYNRTI.TTI.I.TPI.GDSTRRIOESVTTSGGKGKORLIGA 12

12

18

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

[illegible]

C

724

Table 1

Demographic characteristics of study population

N = 60

Age (years)

Mean ± SD

57.8 ± 9.2

Gender

Male

Female

30

30

Ethnicity

Caucasian

African American

Hispanic

Other

45

10

3

2

Education level

High school or less

College

Postgraduate

15

25

20

Marital status

Married

Single

Divorced

Widowed

35

10

10

5

Employment status

Employed

Unemployed

Retired

15

10

35

Income (USD/year)

< \$10,000

\$10,000–\$20,000

\$20,000–\$30,000

> \$30,000

10

15

20

15

Health insurance

Medicare/Medicaid

Private

None

25

25

10

Comorbidities

Hypertension

Diabetes

Cholesterol

Heart disease

Stroke

Arthritis

Depression

Anxiety

15

10

10

10

5

10

10

10

Medication

Antihypertensive

Antidiabetic

Lipid-lowering

Cardiovascular

Psychiatric

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Study site

Urban

Rural

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QY 10C

DD IOT ECECTIVOCYINDECTE

QY
42I RQSCNVLSDDGIETKESGEEDAIQKNVLSIQDQQ : IVCNLSISIDCONVACIGSANTT

DB 42I RQSCNLSLDG T I E R L S G E F D A I I Q N N I S I Q D S Q V I V I G N E D I S I E E C N V A N A C I O C A M E E A S I

QY 481 LEESNSRLDKVNKLTSTISALIIIVLIVISLVCGLSTVJACITMIRQKMQKLEWES QY

Db 481 LEESNSKLDKVNVKLTSTTSALTITYIVLTIVISLVCGILSLVLTACILMINQAKQAKKLEEDG

Qy
541 NNTLDQMRATTKM 553

Db 541 NNTLDQMRATTKM 553

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ABR39678

XX

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XX

XX NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;
KW H-1N1; hemagglutinin; neuraminidase; surface antigen; cancer
therap.; autotaxin gene therap.

XX

OS Newcastle disease virus.
XX
PH Key Location/Qualifiers
FT Misc-difference 1..1103
FT Protein /note= "residues Xaa are encoded by internal stop codons"
FT 1..553
XX /note= "fusion glycoprotein (F)"
XX
PN W02003022202-A2.
XX
XX 20-MAR-2003.
XX
XX 12-SEP-2002; 2002WO-IL000765.
XX
XX 12-SEP-2001; 2001IL-00145397.
XX
XX (YISS) YISSUM RES & DEV CO.
PA (OVCU-) OVURE INC.
XX
XX Zakay-Rones Z, Panet A, Irving C;
XX
XX WPI: 2003-354498/33.
DR N-PSDB; ACC47077.
XX
XX Clonal lentogenic oncolytic strain, particularly a HUJ strain, of
PT Newcastle Disease Virus, useful for treating cancer, comprises a DNA
PT encoding a fusion gene and/or a hemagglutinin-neuraminidase gene.
XX
XX Example; Fig 10; Sipp; English.
XX
XX The invention relates to a clonal lentogenic oncolytic strain of
CC Newcastle Disease Virus (NDV) comprising a DNA sequence encoding for the
CC fusion glycoprotein (F) gene and a part of the haemagglutinin-
CC neuraminidase (HN) gene. The lentogenic oncolytic strain of NDV or a
CC viral glycoprotein having oncolytic activity, is useful in preparing a
CC composition for the treatment of cancer. The present sequence represents
CC a NDV strain HUJ amino acid sequence containing all of the F protein and
XX a partial HN protein
XX
SQ Sequence 1103 AA;

Query Match 95.0%; Score 2620; DB 6; Length 1103;
Best Local Similarity 93.7%; Pred. No. 2.8e-216;
Matches 518; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGSRSSTRIEPLMLTVRVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
DB 1 MGSRPSTKNPAPMLTIRVALALSCICPANSIDGRPLAAGIVTGDKAVNIYTSSQTGS 60

QY 61 IIVKLLPNPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

QY 121 IIGGALGVATAAQITTAASALIQANQANAILRLKERIAATNEAVHEVTDGLSQAVALG 180
DB 121 IIGGVALGVATAAQITTAALALIQANQANAILRLKESIAATNEAVHEVTDGLSQAVALG 180

QY 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNYLTTLTVFGPQIYSPALTIQALYN 240
DB 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNYLTTLTVFGPQIYSPALTIQALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPLVDSQTQALIGIQTLPVSGNLANMRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPLVDSQTQALIGIQTLPVSGNLANMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPMTLKGSVIANCKMTTCRCVNPFGIIISQNYGEAVSLID 420

QY 421 RQSCNVLSLGDITLRLSGEPDATYQKNISODSQVITVGNLIDISTELGNVNSISNALDK 480
DB 421 KQSCNVLSLGGITLRLSGEPDVTYQKNISQVITVGNLIDISTELGNVNSISNALNK 480

QY 481 LEESNSKLDKVNKLTSTLSALITVLTSLVCGILSLVACVLMYKQKAAQKTLMLWG 540
DB 481 LEESNRKLDKVNKLTSTLSALITVLTSLVCGILSLVACVLMYKQKAAQKTLMLWG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 4
AAAY51231
ID AAY51231 standard; protein; 553 AA.
XX
XX AC AAY51231;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Newcastle disease virus LaSota genome encoded protein 4.
XX
XX KW Avian-paramyxovirus; infection; lentogenic; F protein; vaccine;
KW respiratory disease; gastrointestinal disease; poultry pathogen;
KW local immunity.
XX
XX OS Newcastle disease virus.
XX
XX PN W09966045-A1.
XX
XX PD 23-DEC-1999.
XX
XX PF 17-JUN-1999; 99WO-NL000377.
XX
XX PR 19-JUN-1998; 98EP-00202054.
XX
XX PA (DIEN-) STICHTING DIENST LANDBOUEKUNDIG ONDERZOE.
XX
XX PI Peeters BPH, De Leeuw OS, Koch G, Gielkens ALJ;
XX
XX WPI: 2000-106102/09.
XX
XX PT New avian paramyxovirus cDNA, useful for production of vaccine against
PT Newcastle disease virus.
XX
XX PS Disclosure; Fig 3; 115pp; English.
XX
XX CC This invention describes a novel avian-paramyxovirus cDNA (I) which
CC comprises a nucleic acid sequence corresponding to the 5' terminal end of
CC the genome of avian-paramyxovirus allowing the generation of an
CC infectious copy of avian-paramyxovirus. The cell line is useful for the
CC production of infectious lentogenic NDV (Newcastle Disease virus) without
CC the addition of exogenous lentogenic NDV (Newcastle Disease virus) without
CC generate a stable transfected cell line that expresses the wild-type F
CC protein in the virus envelope therefore providing infectious particles,
CC useful in the form of a vaccine, especially against respiratory and/or
CC gastrointestinal diseases. NDV can be easily cultured to very high titers
CC in embryonated eggs. Mass culture of embryonated eggs is relatively
CC cheap. NDV vaccines are relatively stable and can be simply administered
CC by mass application methods e.g. drinking water or by spraying or by
CC aerosol formation. The natural route of infection is by the respiratory
CC and/or gastrointestinal tract which are also the major routes of
CC infection of many other poultry pathogens. NDV can induce local immunity
CC despite the presence of circulating maternal antibody. This sequence
CC represents a protein encoded by the NDV strain LaSota genome which is
CC described in the method of the invention
XX
SQ Sequence 553 AA;

Query Match 94.9%; Score 2616; DB 3; Length 553;
Best Local Similarity 93.5%; Pred. No. 2e-216;
Matches 517; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

New recombinant fowl pox virus for use in vaccines - contains genes expressing antigens of Newcastle disease virus and opt. infectious bronchitis virus.

Disclosure: Page 70-72; 85pp; English.

Newcastle Disease Virus (NDV) HN and F genes were inserted as a SfiI fragment into the homology vector 443-88.8 at the unique SfiI site. The NDV HN and F genes were inserted in the same transcriptional orientation as the ORF in the parental homology vector. The sequence of SfiI fragment is in AAQ68943/R58858/AA859859. The inserted SfiI fragment has the following structure: Junction A - Fragment 1 (HN, AAs 2-577) - Junction B - Fragment 2 (F, AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction D. Fragment 1 is approx. 1811 bp. Fragment 2 is an approx. 1812 bp BamHI to PstI CDNA clone (B1 strain). Fragment 3 is an approx. 1812 bp BamHI to PstI CDNA clone (B1 strain). Fragment 3 is a fragment of the full length NDV F cDNA (B1 Strain). Fragment 3 is an approx. 235 bp PstI and ScaI fragment of the plasmid pBR322. The sequences of the Junctions are in AAQ68945, AAQ68946, AAQ68947, Q68948. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 553 AA:

Query Match 94.7%; Score 2610; DB 2; Length 553;

Best Local Similarity 93.1%; Pred. No. 6.7e-216;

Matches	515;	Conservative	21;	Mismatches	17;	Indels	0;	Gaps	0;
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Qy	1	MGSRSS	TRIPVPLMLTVRVALASCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Db	1	MGRPEST	KNPAPMMLTIRVALJSCIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS	60
Qy	61	IIVKLLPNMP	KDKKACAKAPLEAVNRLLTTLTLPGLDSIRRIQESVTTSGGGQGRLLGA	120
Db	61	IIVKLLPNL	PKDKACAKAPLDANRLLTTLTLPGLDSIRRIQESVTTSGGFRQGRLLGA	120
Qy	121	IIGGAALGV	ATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG	180
Db	121	IIGGVALGV	ATAAQITAAALIQAKNAANILRKESIAATNEAVHEVTDGLSOLAVAVG	180
Qy	181	KMQQFVND	QPNKTAQELDCIKITQOVGVELNLYLTETTVFGQITSPALTQLTICALYN	240
Db	181	KMQQFVND	QPNKTAQELDCIKIAQOVGVELNLYLTETTVFGQITSPALKUKTIOALYN	240
Qy	241	LAGGNMDYLL	TKLGVGNNOISLISGLITGNPILYDSQTQLLGIOVTLPSPVGNLNMRA	300
Db	241	LAGGNMDYLL	TKLGVGNNOISLISGLITGNPILYDSQTQLLGIOVTLPSPVGNLNMRA	300
Qy	301	TYLETLSVST	TKGFASALVPKVMKVGSVIEELDTSYCIETDLDLYCTRIVTTPMPSPGIY	360
Db	301	TYLETLSVST	TRGFASALVPKVTRVGSVIEELDTSYCIETDLDLYCTRIVTTPMPSPGIY	360
Qy	361	SLSGNTSAC	MYSKTEGALTTPYMTLKGSVIANCKMTTCRCAAPPGLIISONYGAEVSLID	420
Db	361	SLSGNTSAC	MYSKTEGALTTPYMTIRKGSVIANCKMTTCRCVPPGLIISONYGAEVSLID	420
Qy	421	ROSCNVLS	LDGTLTLRSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISINALDK	480
Db	421	KQSCNVLS	UGGLTLRSGEFDVTYQKNISIQDSQVIIITGNLDISTELGNVNNISINALNK	480
Qy	481	LBESNKL	DKVNVKLTSTSAIITYIVLTIVSLVCGILSLVLACYLVMYKQAKOQTLILWG	540
Db	481	LBESNRK	DKVNVKLTSTSAIITYIVLTIIISLVFGILSLIACYLVMYKQAKOQTLILWG	540
Qy	541	NNTLDM	RATTQK 553	
Db	541	NNTLDM	RATTQK 553	

RESULT 6

AAR49141

ID AAR49141 standard; protein; 553 AA.

XX

AC AAR49141;

XX

RESULT 5

AA58858

ID: AAR58858 standard; protein; 553 AA.

AC; AAR58858;

XX

DT	25-MAR-2003	(revised)
13	1005	(f)

DT 13-APR-1995 (first entry)

Newcastle Disease Virus F gene product.

NEWCASTLE DISEASE VIRUS F gene product.

SfiI fragment

XX

09 Synthetic.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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PN
yy
WO9419014-A1.

XX
01-SEP-1994XX
01-SEP-1994.

PP 28-FEB-1994

XX

PR 26-FEB-1993; 93.

XX 11

Qy	1	MGSRSTRIPVPLMLITVRVALALSCVCTPSSLDGRPLAAAGIVTGDKAVNIYTSQTGS	60
Db	1	MGSRPSTKNPAPMMITIRVALVLSICIPANSIDGRPLAAAGIVTGDKAVNIYTSQTGS	60
Qy	61	IIVKLLPNWPKDKEACAPLEAYNRTITLTPLGDSIRRIQESVTTSGGCKQRLTGA	120
Db	61	IIVKLLPNLPKDKEACAPLDAYNRTITLTPLGDSIRRIQESVTTSGGGRQRLTGA	120
Qy	121	IIGGAALGVATAAQITTAASALITQANQNAANIURLKERIAATNEAVHEVTDGLSQLAVAG	180
Db	121	IIGGVALGVATAAQITTAALIQAKNAANIURLKESIAATNEAVHEVTDGLSQLAVAG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTQITQALYN	240
Db	181	KMQQFVNDQFNKTAQELDCIKIAQQOVGVNELNLYTESTTVFGPQITSPALNKLTQALYN	240
Qy	241	LAGGNMDYLLFKLGVGNOLSSLIGSLITGNPILYDSOTQLGLQVTLTPSVGNLNNMRA	300
Db	241	LAGGNMDYLLKLGIGNNOLSSLIGSLITGNPILYDSOTQLGLQVTLTPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTRGFASALVPKVTRVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SLCSNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADDPGIIISQNYGEAVSLID	420
Db	361	SLCSNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID	420
Qy	421	QSCNVLSIDGTLRLSGEFDATYOKNISIQDSOVITVGNLDISTELGNVNNSISNALDK	480
Db	421	QSCNVLSLGGITLRLSGEFDVYOKNISIQDSQVITITGNLDISTELGNVNNSISNALNK	480
Qy	481	LEESNKLDKVNVKLTSTSAITYTLTVISLVCGLTSLVACYLMYKQAKQKTLTLWG	540
Db	481	LEESNRKLDKVNVKLTSTSAITYTLTVISLVFGILSLVACYLMYKQAKQKTLTLWG	540
Qy	541	NNTLDDQMRATTQK	553
Db	541	NNTLDDQMRATTQK	553

RESULT 8	
AAW10691	
ID	AAW10691 standard; protein; 553 AA.
XX	
AC	
AAW10691;	
XX	
05-MAY-1997	(first entry)
DT	
XX	
DE	Newcastle disease virus fusion protein.
XX	
FW	Fowlpox virus; FPV; recombinant virus; vector; vaccine; immunisation;
KW	NDV; haemagglutinin; fusion protein; antigen; poultry.
XX	
OS	Newcastle disease virus.
XX	
WO9640880-A1.	
PN	
XX	
PD	19-DEC-1996.
XX	
04-JUN-1996;	96WO-US011187.
XX	
07-JUN-1995;	95US-00484790.
XX	
(SYTR)	SYNTRO CORP.
XX	
Cochran MD,	Junker DE, Singer PA;
XX	
WPI; 1997-087060/08.	
DR	
N-ESDE; AAT48510.	
DR	
XX	
New recombinant fowlpox virus -	contg. a foreign DNA sequence inserted
PT	into the fowlpox virus genome, used for the prodn. of vaccines.
XX	

XX	Disclosure; Page 109-110; 134pp; English.
PS	Newcastle disease virus (NDV) haemagglutinin (HN) (AAW10690) and fusion
XX	(F) protein (AAW10691) are expressed by novel recombinant fowlpox virus
CC	(FPV). The genes (see also AAT48510) for HN and F can be inserted into
CC	homology vector 443-88.8 (see also AAH48511) at the unique Sfil site,
CC	yielding homology vector 502-26.22 (see also AAT48502-05), which can be
CC	used to insert the NDV HN and F genes into fowlpox virus. The recombinant
CC	virus is used to deliver the vaccine antigens to poultry
XX	
SQ	Sequence 553 AA;
	Query Match 94.7%; Score 2610; DB 2; Length 553;
	Best Local Similarity 93.1%; Pred.No.6.7e-216;
	Matches 545; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY	1 MGSRSTRIPVPMLTVRVALALSCVCPTSSLDGRPLAAGIVVTGDKAVNIYTSSQTGS 60
DB	1 MGSRPSTKPNAPMMLIRIVALVLSICIPANSIDGRPLAAGIVVTGDKAVNIYTSSQTGS 60
QY	61 IIVKLIPNPKDKEACAKAPLEAYNRITLTLLTLPGLDSIRRRQESVTTSGGKGQRILGA 120
DB	61 IIVKLIPNPKDKEACAKAPLDAYNRTLTLLTLPGLDSIRRIQESVTTSGGKGQRILGA 120
QY	121 IIGGALGVATAAQITTAASALICANQNAAILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB	121 IIGGVALGVATAAQITTAALAIIOKQNAAILRLKESIATNEAVHEVIDGLSOLAVAVG 180
QY	181 KMQQFVNQDNKTAQELDCIKITQQVGVELNLVLTLTTFVGPQITSPALTOITIQALYN 240
DB	181 KMQQFVNQDNKTAQELDCIKIAQQVGVELNLVLTESTTVFGPQITSPALNKLTIQALYN 240
QY	241 LAGGNMDYLTKLVGNQNQLSSLIGSLITGNPILYDSOTOLLIGIQTLPSPVGNLANMRA 300
DB	241 LAGGNMDYLTKLVGINNQQLSSLIIGSLITGNPILYDSOTOLLIGIQTLPSPVGNLANMRA 300
QY	301 TYLETLSVSTTKGFASALVPKVVMKVGSVIEELDTSYCIETDLDLCTRVITPFPMSPGIY 360
DB	301 TYLETLSVSTTRGFASALVPKVTVRGSVIEELDTSYCIETDLDLCTRVITPFPMSPGIY 360
QY	361 SCLSGNTSAWMYSKTGALTTPWTMLKGVIANCKMTTCRCADPPGIIISONYGEAVSLID 420
DB	361 SCLSGNTSAWMYSKTGALTTPWTMLKGVIANCKMTTCRCVNPFGIISONYGEAVSLID 420
QY	421 RQCNVLSDGITLRLSGEFDATYQKNISTQDSQVI VTGNLDISTELGNVNNISINALDK 480
DB	421 QBCNVLSLGGITLRLSGEFDVYQKNISLODSQVIITGNLDISTELGNVNNISINALNK 480
QY	481 LEESNKKLDKVNKLTSTSAITYIVLTVISLVCGHLSLVACYLMKYKQAOKTLLWLWG 540
DB	481 LEESNRKLDKVNKLTSTSAITYIVLTISIIVFGILSLITACVLYMKYKQAOKTLLWLWG 540
QY	541 NNTLDQMRAATKM 553
DB	541 NNTLDQMRAATKM 553
RESULT 9	
AAAY21983	ID AAY21983 standard; protein; 553 AA.
XX	
AC	AAAY21983;
XX	
DT	07-SEP-1999 (first entry)
XX	
DE	Seq ID No: 14 of US9525358.
XX	
KW	Fowlpox virus; FPV; recombinant; vaccine; immunisation; chicken; NDV;
KW	Newcastle disease virus; NDV; Fowlpox; infectious laryngotracheitis.
XX	
OS	Fowlpox virus.
XX	

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PN US925358-A.
XX
XX
PD 20-JUL-1999.
XX
XX PF 07-JUN-1995; 95US-00484575.
XX
XX PR 26-FEB-1993; 93US-00024156.
XX PR 28-FEB-1994; 94WO-US002252.
XX
XX PA (SYTR ) SYNTRO CORP.
XX
XX PI Junker DE, Cochran MD;
XX
XX DR WPI; 1999-418249/35.
XX DR N-PSDB; AAX81147.
XX
XX PT Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX PT against Fowlpox and Newcastle disease virus.
XX
XX PS Disclosure; Col 61-70; 108pp; English.
XX
XX CC The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX CC foreign DNA inserted into a region of the fowlpox virus genome
XX CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX CC host cell. The virus is used as a vaccine for immunising chickens against
XX CC Newcastle disease virus (NDV), Fowlpox, and infectious Laryngotracheitis
XX CC
XX SQ Sequence 553 AA;

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSRSTRFPVPLMLTRVALALSCVCPPTSSLDGRPLAAAGIVTGDKAIVNTSSQTGS 60
Db 1 MGRSPSTKPNPAPMLTIRVALVSLCPCANSDGRPLAAAGIVTGDKAIVNTSSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRITLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRITLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGALGVATAAQITAAALQANQANANILRLKERIAATNEAVHEVTDGSQLAVAG 180
Db 121 IIGGALGVATAAQITAAALQANQANANILRLKERIAATNEAVHEVTDGSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNYLTETLVFGPQITSPALNKLTICALYN 240
QY 241 LAGGNDYLLTKLGVGNQNLSSLGSLITGNPILYDSOTQLLIGIQTTPSVGNLNNMRA 300
Db 241 LAGGNDYLLTKLIGIGNQLSSLGSLITGNPILYDSOTQLLIGIQTTPSVGNLNNMRA 300
QY 301 TYLETLVSVTTRGFASALVPKVMKGVSVIEELDTSCYETDLDLYCTRTVTPPMSPGIY 360
Db 301 TYLETLVSVTTRGFASALVPKVMKGVSVIEELDTSCYETDLDLYCTRTVTPPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGTILRLSGFEDATYQKNI SIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 KQSCNVSLGGITLRLSGFEDVYQKNI SIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNKLKVNKLTSTALITVIVLTIVSLVCGILSLVLAFLVYKAKOQKTLMLG 540
Db 481 LEESNKLKVNKLTSTALITVIVLTIVSLVCGILSLVLAFLVYKAKOQKTLMLG 540
QY 541 NNTLDQWRATTKM 553
Db 541 NNTLDQWRATTKM 553
```

RESULT 10
AAY58183
ID AAY58183 standard; protein; 553 AA.
XX
XX AAY58183;
AC
XX
DT 14-MAR-2000 (first entry)
XX
XX NDV fusion (F) protein.
XX
XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;
KW infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
KW Marek's disease virus; cytokine; promoter; homologous recombination;
XX homology vector; multivalent; live vaccine; fusion protein.
XX
OS Newcastle disease virus.
XX
XX Key Location/Qualifiers
FH Domain 501..527
FT /note= "Transmembrane anchor domain"
FT
XX
XX US6001369-A.
XX
PD 14-DEC-1999.
XX
XX 07-JUN-1995; 95US-00477459.
XX
XX 26-FEB-1993; 93US-00024156.
PR 28-FEB-1994; 94WO-US002252.
XX
XX (SYTR) SYNTRO CORP.
XX
XX Junker DE, Cochran MD;
PI
XX
XX WPI; 2000-071638/06.
DR
XX
XX N-PSDB; AAZ49295.
XX
Recombinant fowlpox virus useful as a vaccine for immunizing fowl against
PT Marek's disease, Newcastle disease, Infectious Laryngotracheitis Virus
PT and/or fowlpox.
XX
XX Claim 5; Col 71-74; 56pp; English.
XX
The invention relates to a recombinant fowlpox virus (FPV) comprising a
CC foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus
CC genome. The foreign DNA is capable of being expressed in a host cell into
CC which the fowlpox virus has been introduced and encodes an antigenic
CC protein. The antigenic protein which may be expressed includes infectious
CC laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD),
CC AAY58184), Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or
CC fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The
CC foreign DNA may alternatively encode a cytokine such as chicken
CC myelomonocytic growth factor (cMGF) or chicken interferon (cIFN). The
CC foreign DNA in the recombinant FPV is under the control of one or more
CC synthetic pox promoters, enabling control of strength and timing of
CC heterologous gene expression. The synthetic pox virus promoters that may
CC be used are based on promoters of the vaccinia virus and include early
CC promoter 1 (EPI), late promoter 1 (LPI), EP2 and LP2 (AAZ49291-249294,
CC respectively). The recombinant FPV is generated via homologous
CC recombination between FPV DNA and a homology vector containing the
CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
CC the invention are used as multivalent live vaccines for immunising fowl
CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
CC present sequence represents NDV fusion (F) protein
XX
XX Sequence 553 AA;
SQ

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSRSTRFPVPLMLTRVALALSCVCPPTSSLDGRPLAAAGIVTGDKAIVNTSSQTGS 60

QY 61 IIVKLLNPKDKKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
 Db 61 IIVKLLNPKDKKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 Db 121 IIGSVLGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
 Db 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
 QY 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLCTRIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKWTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKWTCRCADPPGIISQNYGEAVSLID 420
 QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLDISTELGNVNNISNALDK 480
 Db 421 RHSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLDISTELGNVNNISNALDK 480
 QY 481 LEESNSKLDKVNKLTSTTSALITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLMLG 540
 Db 481 LEESNSKLDKVNKLTSTTSALITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLMLG 540
 QY 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKI 553

RESULT 14

AAP70176
 ID AAP70176 standard; protein; 553 AA.

AC AAP70176;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 03-APR-1991 (first entry)

DE Sequence of Newcastle Disease Virus (NDV) F polypeptide.

KW Epitope; probe; diagnosis.

OS Newcastle disease virus.

XX EP227414-A.

XX 01-JUL-1987.

XX 16-DEC-1986; 86EP-00309804.

XX 18-DEC-1985; 85GB-00031147.

XX 14-APR-1986; 86GB-00009037.

XX 15-JUL-1986; 86US-00885765.

XX (NATR) NAT RES DEV CORP.

XX Bingham RW, Chambers P, Emmerson PT, Millar NS;

XX WPI; 1987-179630/26.

XX N-PSDB; AAN70261.

XX Newcastle disease virus gene clones - comprise polynucleotide(s) encoding
 PT the HN and/or F protein of Newcastle disease virus RNA.

XX Example; Page 11-16; 22pp; English.
 XX An artificial polynucleotide encoding an HN and/or F polypeptide of
 CC Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or
 CC an epitopic portion of the polypeptide or an artificial nucleotide
 CC complementary to the polynucleotide are claimed. The polynucleotides are
 CC useful for preparing a probe for extracting similar genes from a gene
 CC library or for identifying the presence of NDV virions in a sample obcd.
 CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 27-AUG-2003 to correct OS field.)

XX Sequence 553 AA;

Query Match 94.4%; Score 2603; DB 1; Length 553;
 Best Local Similarity 93.5%; Pred. No. 2.7e-215;
 Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 Db 1 MGRPRSTKNPVPVMTLTVRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYTSQTGS 60
 QY 61 IIVKLLNPKDKKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
 Db 61 IIVKLLNPKDKKACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGAALGVATAAQTAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 Db 121 IIGVGVATAAQTAAALIQAKNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTELTTVFGPQITSPALTIQALYN 240
 Db 181 KMQQFVNDQFNKTAQELGCIIRIAQQGVGVELNLYLTTELTTVFGPQITSPALNKLTQALYN 240
 QY 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTRGFASALVPKVTQVGSVIEBELDTSYCIETDLDLCTRIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKWTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMSYKTEGALTTPYMTIKGSVIANCKWTCRCVNPPIISQNYGEAVSLID 420
 QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLDISTELGNVNNISNALDK 480
 Db 421 KQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNALNK 480
 QY 481 LEESNSKLDKVNKLTSTTSALITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLMLG 540
 Db 481 LEESNSKLDKVNKLTSTTSALITYVLTIVSLVCGILSLVACVLMYKQKQAKTLLMLG 540
 QY 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKM 553

RESULT 15

ABG31709
 ID ABG31709 standard; protein; 564 AA.

XX ABG31709;

XX 15-NOV-2002 (first entry)

XX Newcastle disease virus (NDV) fusion protein.

XX Newcastle disease virus; NDV; novel recombinant avian herpesvirus; NAHV;
 XX herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
 KW infectious laryngotracheitis; virucide; immunostimulant; vaccine.
 XX

252 LAGNMDYLLTKLGIGNNOI

OS	Newcastle disease virus.
XX	
FX	Key Location/Qualifiers
FF	Misc-difference 54
FT	/label= unknown
FT	/note= "Encoded by CTN"
XX	
PN	US2002081316-A1.
XX	
PD	27-JUN-2002.
XX	
PF	14-JUN-2001; 2001US-00881457.
XX	
PR	12-JUN-1992; 92US-00898087.
PR	26-FEB-1993; 93US-00023610.
PR	14-JUN-1993; 93WO-US005681.
PR	09-AUG-1994; 94US-00288065.
PR	09-AUG-1995; 95WO-US010245.
PR	13-JUN-1996; 96US-00663566.
PR	21-FEB-1997; 97US-00804372.
PR	25-OCT-1999; 99US-00426352.
XX	
PA	(COCH/) COCHRAN M D.
PA	(COOK/) COOK S M.
PA	(WILD/) WILD M A.
XX	
PI	Cochran MD, Cook SM, Wild MA;
XX	
DR	WPI; 2002-635456/68.
DR	N-PSDB; ABK90556.
XX	
PT	Novel recombinant avian herpesvirus comprising unique long and repeat
PT	viral genome regions of herpes virus of turkeys, unique short viral
PT	genome region of Marek's disease virus, and optional foreign DNA
PT	sequence.
XX	
PS	Disclosure; Page 14-16; 26pp; English.
XX	
CC	The invention relates to a novel recombinant avian herpesvirus (NAHV)
CC	comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat
CC	viral genome region and a Marek's disease virus unique short (US) viral
CC	genome region where at least one foreign DNA sequence is inserted within
CC	a US2 gene of the US region of the NAHV, and is capable of being
CC	expressed in a host cell. NAHV is useful for producing vaccines used for
CC	immunising an avian species against Newcastle disease, infectious
CC	laryngotracheitis and Marek's disease. This sequence represents a
CC	Newcastle disease virus (NDV) fusion protein
XX	
SQ	Sequence 564 AA;
	Query Match 90.4%; Score 2493.5; DB 5; Length 564;
	Best Local Similarity 89.7%; Pred.No. 7.8e-206;
	Matches 496; Conservative 24; Mismatches 32; Indels 1; Gaps 1;
QY	1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTGS 60
Db	13 MGRSEPKNPAPMMLTIRVALVLSICIFANSIDGRPLAAGXWLQETKQ-STYTEHPQV 71
QY	61 IIVKLNNMPKDKEACAKAPLEAYNRITLTLLTPLGDSIRRIQESVTTSGGKGQRLLIGA 120
Db	72 NHIKLLENLPDKEACAKAPLDAYNRITLTLLTPLGDSIRRIQESVTTSGGKGQRLLIGA 131
QY	121 IIGGAALGVATAAQITASALTIQANQNANTILRLKERTAAATNEAVEHVTDLGLSOLAVVG 180
Db	132 IIGGVALGVATAAQITAAAALIQAQNAANTILRLKESAAATNEAVEHVTDLGLSOLAVVG 191
QY	181 KMQQFVNDFNKTAQELDCIKITQQVGVNELNYLTTELTTVPQPITSPALTOLTTCALYN 240
Db	192 KMQQFVNDFNKTAQELDCIKIAQQVGVNELNYLTTESTVFPQITSPALKLTTCALYN 251
QY	241 LAGNM DYLLTKLVGNVNQLSSLIGSGIITGNPILYDSQTOLLGHIOVLTPSVGNLNMMRA 300
Db	252 LAGNM DYLLTKLVGINNQLSSLIGSGIITGNPILYDSQTOLLGHIOVLTPSVGNLNMMRA 311

	Qy	301	TYLETISVSTTKGFASALVPKVWVKGSVIBELDTSYCIETDLDYCTRIVTFFPMSPGII	360
			: : : :	
	Db	312	TYLETISVSTRGFASALVPKVVTRGVSIVBELDTSYCIETDLDYCTRIVTFFPMSPGII	371
			: : : :	
	Qy	361	SCLSGNTSACWYSKTEGALTTPMYTLKGSVIANCKWTTCRCADPPGIIISQNYGEAVSLID	420
			: : : :	
	Db	372	SCLSGNTSACWYSKTEGALTTPMYTLKGSVIANCKWTTCRCVNPFGIIISQNYGEAVSLID	431
			: : : :	
	Qy	421	RQSCNVLSLGGITILRLSGEFPATYQKNISIQDSQVIVTGNIJDISTELGNVNNSISNALDK	480
			: : : : : :	
	Db	432	KQSCNVLSLGGITILRLSGEFPATYQKNISIQDSQVITGNIJDISTELGNVNNSISNALNK	491
			: : : :	
	Qy	481	LEESNKLKDKNVKILTSTALITYVLTVTLVLGVGLSLVLACYLMYKQAKOQTLLWLIG	540
			: : : :	
	Db	492	LEESNKLKDKNVKILTSTALITYVLTVTLVLGVGLSLVLACYLMYKQAKOQTLLWLIG	551
			: : : :	
	Qy	541	NNTLDQMRAATTKM	553
			: : : :	
	Db	552	NNTLDQMRAATTKM	564
			: : : :	

Search completed: April 18, 2004, 01:23:38
Job time : 103 secs

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Result No.	Query	Score	Match	Length	DB	ID	Description	
1	2610	94.7	553	2	US-08-663-566A-13	Sequence 13, Appl		
2	2610	94.7	553	2	US-08-484-575A-14	Sequence 14, Appl		
3	2610	94.7	553	2	US-08-023-610-13	Sequence 13, Appl		
4	2610	94.7	553	2	US-08-288-065A-13	Sequence 13, Appl		
5	2610	94.7	553	2	US-08-362-240A-13	Sequence 13, Appl		
6	2610	94.7	553	3	US-08-477-459-14	Sequence 14, Appl		
7	2610	94.7	553	3	US-08-479-869-14	Sequence 14, Appl		
8	2610	94.7	553	3	US-08-486-414-14	Sequence 14, Appl		
9	2610	94.7	553	5	US-08-804-372A-11	Sequence 11, Appl		
10	2610	94.7	553	5	PCT-US94-01826A-14	Sequence 14, Appl		
11	2610	94.7	553	5	PCT-US94-02252A-14	Sequence 14, Appl		
12	2610	94.7	553	5	PCT-US95-10245-13	Sequence 13, Appl		
13	2572	93.3	553	6	5310678-1	Patent No. 5310678		
14	2086.5	75.7	436	3	US-08-486-099-94	Sequence 94, Appl		
15	2086.5	75.7	436	3	US-08-360-107A-104	Sequence 104, Appl		
16	2086.5	75.7	436	3	US-08-484-232B-94	Sequence 94, Appl		
17	2086.5	75.7	436	3	US-08-919-597-94	Sequence 94, Appl		
18	2086.5	75.7	436	3	US-08-475-688A-94	Sequence 94, Appl		
19	2086.5	75.7	436	3	US-08-485-551A-94	Sequence 94, Appl		
20	2086.5	75.7	436	3	US-08-471-913A-94	Sequence 94, Appl		
21	2086.5	75.7	436	3	US-08-485-264A-94	Sequence 94, Appl		
22	2086.5	75.7	436	4	US-08-474-349A-94	Sequence 94, Appl		
23	2086.5	75.7	436	4	US-08-255-208A-30	Sequence 30, Appl		
24	2086.5	75.7	436	4	US-08-470-896-94	Sequence 30, Appl		
25	2086.5	75.7	436	4	US-08-485-546A-94	Sequence 94, Appl		
26	712	25.8	551	2	US-08-700-548-94	Sequence 94, Appl		
27	689	25.0	542	1	US-08-321-587-2	Sequence 2, Appl		

		Query Match		94.7%: Score 2610; DB 2; Length 553;	
		Best Local Similarity		93.1%: Pred. No. 3,2e-230;	
		Matches 515; Conservative		21; Mismatches 17; Indels 0; Gaps 0;	
Qy	1	MGRSSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGKAVNIYTSSTGTS	60		
Db	1	MGRSPSTKPNPWWLTIRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYTSSTGTS	60		
Qy	61	IIVKLLNPKDKKACAKAPLEAYNRLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA	120		
Db	61	IIVKLLNPKDKKACAKAPLEAYNRLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA	120		
Qy	121	IIGAAALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSLAVAVG	180		
Db	121	IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSLAVAVG	180		
Qy	181	KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTELTTVPFPOITSPALTIQALYN	240		
Db	181	KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTESTTVPFPOITSPALNKLTIOALYN	240		
Qy	241	LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIQVTLPSVGNLNNMRA	300		
Db	241	LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIQVTLPSVGNLNNMRA	300		
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360		
Db	301	TYLETLSVSTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360		
Qy	361	SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID	420		
Db	361	SCLSGNTSACMYSTEGALTPPYMTIKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID	420		
Qy	421	ROSCNVLSLGGITLRLSGERDATYQKNISIODSOVITVGNLDISTELGNVNNISNALDK	480		
Db	421	KQSCNVLSLGGITLRLSGEFVDTYQKNISIODSVIITGNLDISTELGNVNNISNALNK	480		
Qy	481	LEENSKLDKVNKLITSTALITYIVLTVISLVCGILSLVACLYMYKQKQKTLMLWG	540		
Db	481	LEENSKLDKVNKLITSTALITYIVLTIISLVFGILSLIACLYMYKQKQKTLMLWG	540		
Qy	541	NNTLDQMRATTKM	553		
Db	541	NNTLDQMRATTKM	553		

		Query Match		94.7%: Score 2610; DB 2; Length 553;	
		Best Local Similarity		93.1%: Pred. No. 3,2e-230;	
		Matches 515; Conservative		21; Mismatches 17; Indels 0; Gaps 0;	
Qy	1	MGRSSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVVTGKAVNIYTSSTGTS	60		
Db	1	MGRSPSTKPNPWWLTIRVALVLSICIPANSIDGRPLAAAGIVVTGKAVNIYTSSTGTS	60		
Qy	61	IIVKLLNPKDKKACAKAPLEAYNRLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA	120		
Db	61	IIVKLLNPKDKKACAKAPLEAYNRLTLLTLPGLDSIRRIQESVTTSGGKQGRLLIGA	120		
Qy	121	IIGAAALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSLAVAVG	180		
Db	121	IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSLAVAVG	180		
Qy	181	KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTELTTVPFPOITSPALTIQALYN	240		
Db	181	KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTESTTVPFPOITSPALNKLTIOALYN	240		
Qy	241	LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIQVTLPSVGNLNNMRA	300		
Db	241	LAGNMVLLTKLGVGNQSSLLGSLITGNPILYDSOTOLLGIQVTLPSVGNLNNMRA	300		
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360		
Db	301	TYLETLSVSTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY	360		
Qy	361	SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID	420		
Db	361	SCLSGNTSACMYSTEGALTPPYMTIKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID	420		
Qy	421	ROSCNVLSLGGITLRLSGERDATYQKNISIODSOVITVGNLDISTELGNVNNISNALDK	480		
Db	421	KQSCNVLSLGGITLRLSGEFVDTYQKNISIODSVIITGNLDISTELGNVNNISNALNK	480		
Qy	481	LEENSKLDKVNKLITSTALITYIVLTVISLVCGILSLVACLYMYKQKQKTLMLWG	540		
Db	481	LEENSKLDKVNKLITSTALITYIVLTIISLVFGILSLIACLYMYKQKQKTLMLWG	540		
Qy	541	NNTLDQMRATTKM	553		
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RESULT 3

US-08-023-610-13

Sequence 13, Application US/08023610

Patent No. 5928648

GENERAL INFORMATION:

APPLICANT: Cochran Ph.D., Mark D

APPLICANT: Macdonald Ph.D., Richard D

TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

TITLE OF INVENTION: and Uses Thereof

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSER: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,575A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White Esq, John P

TELEPHONE: (212)278-0450

TELEFAX: (212)391-0525

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-484-575A-14

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-023-610-13

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVG 180
DB 121 IIGGVALGVATAAQITAAALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTKTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTKTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESSNKLKDVNKLSTSTALITYIVLTIVISLVCGILSLVACVLMYKQKQKTLILWL 540
DB 481 LEESSNKLKDVNKLSTSTALITYIVLTIVISLVCGILSLVACVLMYKQKQKTLILWL 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 4
US-08-288-065A-13
; Sequence 13, Application US/08288065A
; Patent No. 5961982
GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; TITLE OF INVENTION: HVT-050 and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,065A
FILING DATE: Aug-09-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-065A-13

Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTGS 60
QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAQITAAALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVG 180
DB 121 IIGGVALGVATAAQITAAALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTKTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTKTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGEFDTYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESSNKLKDVNKLSTSTALITYIVLTIVISLVCGILSLVACVLMYKQKQKTLILWL 540
DB 481 LEESSNKLKDVNKLSTSTALITYIVLTIVISLVCGILSLVACVLMYKQKQKTLILWL 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 5
US-08-362-240A-13
; Sequence 13, Application US/08362240A
; Patent No. 5965138

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GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-240A-13

Query Match          94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Db 1 MGRSPSTKPNPMMLTIRVALVLCICPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDKKAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIOAKNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGGVALGVATAAQITAAALIOAKNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALQTLTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTETLTVFGPQITSPALNKLTIQALYN 240
Qy 241 LAGGNMAYLLKLGNNQLSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNNMRA 300
Db 241 LAGGNMAYLLKLGNNQLSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
Qy 421 ROSCNVLSIDGTLRLSGEFDATYOKNISIQDSQVIVTCNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSIDGTLRLSGEFDFYOKNISIQDSQVIVTCNLIDISTELGNVNNISNALNK 480

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-459-14

Query Match          94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Db 1 MGRSPSTKPNPMMLTIRVALVLCICPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDKKAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIOAKNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGGVALGVATAAQITAAALIOAKNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALQTLTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTETLTVFGPQITSPALNKLTIQALYN 240
Qy 241 LAGGNMAYLLKLGNNQLSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNNMRA 300
Db 241 LAGGNMAYLLKLGNNQLSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
Qy 421 ROSCNVLSIDGTLRLSGEFDATYOKNISIQDSQVIVTCNLIDISTELGNVNNISNALDK 480
Db 421 ROSCNVLSIDGTLRLSGEFDFYOKNISIQDSQVIVTCNLIDISTELGNVNNISNALNK 480
```

Db 301 TYLETSLVSTTRGFASALVPKVVTRVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGDITLRLSGEFDVTVQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVACVLYMYKQKAAQKTLWLIG 540
Db 481 LEESNRKLDKVNKLTSTLSALITYIVLTIVSLVFGILSLVACVLYMYKQKAAQKTLWLIG 540
QY 541 NNTLDQWRATTM 553
Db 541 NNTLDQWRATTM 553

RESULT 7

US-08-479-869-14
; Sequence 14, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D, Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-869-14

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSOTGS 60
Db 1 MGRSPSTKNPAPWMLTIRVALVLSLSCIPANSIDGRPLAAAGIVTGDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLIGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLIGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQGVGVELNLVLTETTVFGPQITSPALNKLTIOALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGIQVTLFSPVGNLNMRA 300
Db 241 LAGNMDYLLTKLIGGNQLSSLIGSLITGNPILYDSQTLGLIGIQVTLFSPVGNLNMRA 300
QY 301 TYLETSLVSTTRGFASALVPKVVTRVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTRGFASALVPKVVTRVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGDITLRLSGEFDVTVQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTLSALITYIVLTIVSLVCGILSLVACVLYMYKQKAAQKTLWLIG 540
Db 481 LEESNRKLDKVNKLTSTLSALITYIVLTIVSLVFGILSLVACVLYMYKQKAAQKTLWLIG 540
QY 541 NNTLDQWRATTM 553
Db 541 NNTLDQWRATTM 553

RESULT 8

US-08-486-414-14
; Sequence 14, Application US/08486414B
; Patent No. 6136318
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
; FILE REFERENCE: 42771D
; CURRENT APPLICATION NUMBER: US/08/486,414B
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Fowlpox virus
US-08-486-414-14

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSOTGS 60
Db 1 MGRSPSTKNPAPWMLTIRVALVLSLSCIPANSIDGRPLAAAGIVTGDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLIGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLIGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGVALGVATAAQITAAALIQAKQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLVLTETTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQGVGVELNLVLTETTVFGPQITSPALNKLTIOALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGIQVTLFSPVGNLNMRA 300

Db 241 LAGNMDVLLKLGIGNNQLSSLGITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIODSQVIVITGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIODSQVIVITGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACYLIMYKQKQAKQKTLMLIG 540
Db 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACYLIMYKQKQAKQKTLMLIG 540
QY 541 NNTLDMOERATTKM 553
Db 541 NNTLDMOERATTKM 553

RESULT 9

US-08-804-372A-11
; Sequence 11, Application US/08804372A
; Patent No. 6183753
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Wild, Martha A.
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,372A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 2552/39115E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-804-372A-11

Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGSRSSTRPVLMLTVRVALSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSSTQGS 60
Db 1 MGSRPSTKNPAPMMLTIRVALVLSICPCPANSIDGRPLAAGIVVTGDKAVNIYTSSTQGS 60

QY 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSQLAVAVG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVVELNLYLTETTVFGPQITSPALTKLTIQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKITQOVGVVELNLYLTETTVFGPQITSPALTKLTIQALYN 240
QY 241 LAGNMDVLLKLGIGNNQLSSLGITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
Db 241 LAGNMDVLLKLGIGNNQLSSLGITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGVSIVANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIODSQVIVITGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIODSQVIVITGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACYLIMYKQKQAKQKTLMLIG 540
Db 481 LEESNKLDKVNKLTSTTSALITYIVLVISVCGILSLVACYLIMYKQKQAKQKTLMLIG 540
QY 541 NNTLDMOERATTKM 553
Db 541 NNTLDMOERATTKM 553

RESULT 10
PCT-US94-01826A-14
; Sequence 14, Application PC/TUS9401826A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US94-01826A-14

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAANEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAASALIQANQANANILRLKERIAANEAVHEVTDGLSOLAVAG 180

QY 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTIOALYN 240
DB 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTIOALYN 240

QY 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIQDSQVITGNLIDISTELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTALITYIVLTVISLVCGILSLVLACVLYMKQAKOQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITYIVLTVISLVFGILSLILACVLYMKQAKOQKTLWLIG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 11

PCT-US94-02252A-14
; Sequence 14, Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Synro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq. John P
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-02252A-14

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGRSPSTKNPAPMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANANILRLKERIAANEAVHEVTDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAASALIQANQANANILRLKERIAANEAVHEVTDGLSOLAVAG 180

QY 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTIOALYN 240
DB 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTIOALYN 240

QY 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQNLSSGLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLGDITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLGGITLRLSGEFDVYQKNISIQDSQVITGNLIDISTELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTALITYIVLTVISLVCGILSLVLACVLYMKQAKOQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITYIVLTVISLVFGILSLILACVLYMKQAKOQKTLWLIG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 12

PCT-US95-10245-13
; Sequence 13, Application PC/TUS9510245
; GENERAL INFORMATION:
; APPLICANT: SYNTRO CORPORATION
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10245
FILING DATE: 09-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-10245-13

Query Match 94.7%; Score 2610; DB 5; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.2e-230;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTVGDKAVNIYTSSTG 60
DB 1 MGRPSTKNPAPMLTIIRVALVLSICIPANSIDGRPLAAAGIVTVGDKAVNIYTSSTG 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNPKDKEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGALGVATAAQTAAALIQANQNAANILRLKERTAAATNEAVHEVTDGLSQLAVAG 180
DB 121 IIGGVALGVATAAQTAAALIQANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVLELNLYLTETTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVLELNLYLTETTVFGPQITSPALNKLTITQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTLQGLIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTLQGLIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCWMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCWMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLDGITLRLSGEFDYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNVKLTSTALITYIVLTIVISVCGILSLVLACYLMYKQAKQKTLMLIG 540
DB 481 LEESNRKLDKVNKLTSTALITYIVLTIIISLVFGILSLVLACYLMYKQAKQKTLMLIG 540
QY 541 NNTLDQMRATTQM 553
DB 541 NNTLDQMRATTQM 553

RESULT 13
5310678-1
; Patent No. 5310678
; APPLICANT: Bingham, Richard W.; Chambers, Philip; Emmerson, Peter
; T.; Miller, Neil S.
; TITLE OF INVENTION: NEWCASTLE DISEASE VIRUS GENE CLONES
; NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/438,945
FILING DATE: 17-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 885,765
FILING DATE: 15-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 553
5310678-1

Query Match 93.3%; Score 2572; DB 6; Length 553;
Best Local Similarity 92.8%; Pred. No. 9.8e-227;
Matches 513; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTVGDKAVNIYTSSTG 60
DB 1 MGRPSTKNPVPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVTVGDKAVNIYTSSTG 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNPKDKEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQRLIGA 120
QY 121 IIGGALGVATAAQTAAALIQANQNAANILRLKERTAAATNEAVHEVTDGLSQLAVAG 180
DB 121 IIGGVALGVATAAQTAAALIQANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVLELNLYLTETTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVLELNLYLTETTVFGPQITSPALNKLTITQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTLQGLIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTLQGLIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTRGFASALVPKVVTRVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCWMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCWMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
DB 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNVKLTSTALITYIVLTIVISVCGILSLVLACYLMYKQAKQKTLMLIG 540
DB 481 LEESNRKLDKVNKLTSTALITYIVLTIIISLVFGILSLVLACYLMYKQAKQKTLMLIG 540
QY 541 NNTLDQMRATTQM 553
DB 541 NNTLDQMRATTQM 553

RESULT 14
US-08-486-099-94
; Sequence 94, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,099
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-031
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 94:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 436 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-486-099-94

Query Match 75.7%; Score 2086.5; DB 3; Length 436;
 Best Local Similarity 96.6%; Pred. No. 1.9e-182;
 Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;
 QY 118 IGAIIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAV 177
 DB 2 IGAIIGSVLGVATAAQITAAASALIQANQNAANILRLKESITATIEAVHEVTDGLSOLAV 61
 QY 178 AVGKMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIA 237
 DB 62 AVGKMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIA 121
 QY 238 LYNLAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNN 297
 DB 122 LYN-AGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNN 180
 QY 298 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSP 357
 DB 181 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSP 240
 QY 358 GIYSCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
 DB 241 GIYSCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
 QY 418 LIDRQSCNVLSLGDITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNNISNA 477
 DB 301 LIDRHSCNVLSLGDITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNNISNA 360
 QY 478 LDKLEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVACLYMYKQKQAQKTL 537
 DB 361 LDKLEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVACLYMYKQKQAQKTL 420
 QY 538 WLGNTLDQMRATTKM 553
 DB 421 WLGNTLDQMRATTKM 436

RESULT 15

US-08-360-107A-104
 ; Sequence 104, Application US/08360107A
 ; Patent No. 6017536
 ; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 ; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; TITLE OF INVENTION: TRANSMISSION
 ; NUMBER OF SEQUENCES: 149
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,107A
 ; FILING DATE: 20-DEC-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-013
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 104:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 436 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-360-107A-104

Query Match 75.7%; Score 2086.5; DB 3; Length 436;
 Best Local Similarity 96.6%; Pred. No. 1.9e-182;
 Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;
 QY 118 IGAIIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAV 177
 DB 2 IGAIIGSVLGVATAAQITAAASALIQANQNAANILRLKESITATIEAVHEVTDGLSOLAV 61
 QY 178 AVGKMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIA 237
 DB 62 AVGKMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTETTVFGPOITSPALTLTQIA 121
 QY 238 LYNLAGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNN 297
 DB 122 LYN-AGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNN 180
 QY 298 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSP 357
 DB 181 MRATYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSP 240
 QY 358 GIYSCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
 DB 241 GIYSCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
 QY 418 LIDRQSCNVLSLGDITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNNISNA 477
 DB 301 LIDRHSCNVLSLGDITLRLSGEFDATYQKNSIQDSQVIVTGNLDISTELGNVNNISNA 360
 QY 478 LDKLEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVACLYMYKQKQAQKTL 537

Db 361 LDKLEESNSKLDKVNKLTSTISALITYTALTATISLVCGILSVLACYLMYKQKQKTL 420
Qy 538 WLGNTLQMRATTOM 553
Db 421 WLGNTLQMRATTOM 436

Search completed: April 18, 2004, 02:34:36
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:23:45 ; Search time 81 Seconds
(without alignments)
1882.065 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSRSTRPVPMLTVRVA.....XTLLWLGNTLDQMRATYTM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2493.5	90.4	564	9 US-09-881-457A-2	Sequence 2, Appli
2	2086.5	75.7	436	12 US-10-267-682-94	Sequence 94, Appl
3	2086.5	75.7	436	12 US-10-267-748-94	Sequence 94, Appl
4	623.5	22.6	662	10 US-09-951-061A-141	Sequence 141, App
5	621.5	22.5	662	12 US-10-670-695-36	Sequence 36, Appl
6	606.5	22.0	550	9 US-09-873-233A-20	Sequence 18, Appl
7	605.5	22.0	550	9 US-09-873-233A-18	Sequence 18, Appl
8	534	19.4	438	12 US-10-267-682-93	Sequence 93, Appl
9	534	19.4	438	12 US-10-267-748-93	Sequence 93, Appl
10	504	18.3	438	12 US-10-267-682-105	Sequence 105, App
11	504	18.3	438	12 US-10-267-748-105	Sequence 105, App
12	458	16.6	430	12 US-10-267-682-95	Sequence 95, Appl
13	458	16.6	430	12 US-10-267-748-95	Sequence 95, Appl
14	211	7.7	574	15 US-10-371-264-6	Sequence 6, Appli
15	211	7.7	574	15 US-10-371-099-6	Sequence 6, Appli

16	211	7.7	574	15	US-10-371-122-6	Sequence 6, Appli
17	211	7.7	574	15	US-10-373-567-6	Sequence 6, Appli
18	210.5	7.6	539	15	US-10-371-264-19	Sequence 19, Appl
19	210.5	7.6	539	15	US-10-371-099-315	Sequence 315, App
20	210.5	7.6	539	15	US-10-371-122-315	Sequence 315, App
21	210.5	7.6	539	15	US-10-373-567-19	Sequence 19, Appl
22	208.5	7.6	539	15	US-10-371-264-9	Sequence 9, Appli
23	208.5	7.6	539	15	US-10-371-264-18	Sequence 18, Appl
24	208.5	7.6	539	15	US-10-371-099-9	Sequence 9, Appli
25	208.5	7.6	539	15	US-10-371-099-314	Sequence 314, App
26	208.5	7.6	539	15	US-10-371-122-9	Sequence 9, Appli
27	208.5	7.6	539	15	US-10-371-122-314	Sequence 314, App
28	208.5	7.6	539	15	US-10-373-567-9	Sequence 9, Appli
29	208.5	7.6	539	15	US-10-373-567-18	Sequence 18, Appl
30	203	7.4	574	15	US-10-371-264-7	Sequence 7, Appli
31	203	7.4	574	15	US-10-371-099-7	Sequence 7, Appli
32	203	7.4	574	15	US-10-371-122-7	Sequence 7, Appli
33	203	7.4	574	15	US-10-373-567-7	Sequence 7, Appli
34	198.5	7.2	539	15	US-10-371-264-21	Sequence 21, Appl
35	198.5	7.2	539	15	US-10-371-099-317	Sequence 317, App
36	198.5	7.2	539	15	US-10-371-122-317	Sequence 317, App
37	198.5	7.2	539	15	US-10-373-567-21	Sequence 21, Appl
38	194	7.0	538	15	US-10-371-264-12	Sequence 12, Appl
39	194	7.0	538	15	US-10-371-099-12	Sequence 12, Appl
40	194	7.0	538	15	US-10-371-122-12	Sequence 12, Appl
41	194	7.0	538	15	US-10-373-567-12	Sequence 12, Appl
42	192.5	7.0	539	15	US-10-371-264-20	Sequence 20, Appl
43	192.5	7.0	539	15	US-10-371-099-316	Sequence 316, App
44	192.5	7.0	539	15	US-10-371-122-316	Sequence 316, App
45	192.5	7.0	539	15	US-10-373-567-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

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US-09-881-457A-2
; Sequence 2, Application US/09881457A
; Patent No. US20020081316A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Cook, Stephanie M
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: No. US20020081316A1e1 Avian Herpes Virus and Uses Thereof
; FILE REFERENCE: SY01105K1QKQK
; CURRENT APPLICATION NUMBER: US/09/881,457A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/426,352
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/804,372
; PRIOR FILING DATE: 1997-02-21
; PRIOR APPLICATION NUMBER: PCT/US95/10245
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: 08/663,566
; PRIOR FILING DATE: 1996-06-13
; PRIOR APPLICATION NUMBER: 08/288,065
; PRIOR FILING DATE: 1994-08-09
; PRIOR APPLICATION NUMBER: PCT/US93/05681
; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: 08/023,610
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/898,087
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Newcastle disease virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (54)-
; OTHER INFORMATION: Xaa = any amino acid

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US-09-881-457A-2

Query Match 90.4%; Score 2493.5; DB 9; Length 564;
Best Local Similarity 89.7%; Pred. No. 3.2e-207;
Matches 496; Conservative 24; Mismatches 32; Indels 1; Gaps 1;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGKAVNIYTSQTGS 60
DB 13 MGRSPSTKNPAPMMLTVIRVALVLSICIPANSIDGRPLAAGXWLOETKQ-STYTPHPQV 71
QY 61 IIVKLLPNMPKDXEACAPLEAYNRTLTLLTPLGDSIRRIQSVTSSGGKQGRIGA 120
DB 72 NHKLLPNLPKDXEACAPLDAYNRTLTLLTPLGDSIRRIQSVTSSGGKQGRIGA 131
QY 121 IIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAV 180
DB 132 IIGGVALGVATAAQITAAALIQANNAANILRLKESIAATNEAVHEVTDGLSOLAV 191
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALQTQIA 240
DB 192 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALNKLTIQ 251
QY 241 LAGNMDYLLTKLGVNNQSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNMRA 300
DB 252 LAGNMDYLLTKLGVNNQSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNMRA 311
QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIBELDTSYCIETDLYCTRIVTFPMSPGIY 360
DB 312 TYLETLSVTTKGFASALVPKVMKGVSVIBELDTSYCIETDLYCTRIVTFPMSPGIY 371
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAV 420
DB 372 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAV 431
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNAL 480
DB 432 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNAL 491
QY 481 LEESNKLKDVNKLKTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 540
DB 492 LEESNKLKDVNKLKTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 551
QY 541 NNTLDQMRATTKM 553
DB 552 NNTLDQMRATTKM 564

RESULT 2
US-10-267-682-94
Sequence 94, Application US/10267682
Publication No. US2004003235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Pettaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: unknown
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 94:

US-10-267-682-94

Query Match 75.7%; Score 2086.5; DB 12; Length 436;

Best Local Similarity 96.6%; Pred. No. 4.3e-172;
Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 118 IGATIGGAALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAV 177
DB 2 IGATIGGVALGVATAAQITAAALIQANNAANILRLKESITATIEAVHEVTDGLSOLAV 61
QY 178 AVGRMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALQTQIA 237
DB 62 AVGRMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALQTQIA 121
QY 238 LYNLAGNMDYLLTKLGVNNQSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNM 297
DB 122 LYN-AGNMDYLLTKLGVNNQSLIGSLITGNPIYDSQTLGLGIVTLPSVGNLNM 180
QY 298 MRATYLETLSVTTKGFASALVPKVMKGVSVIBELDTSYCIETDLYCTRIVTFPMSP 357
DB 181 MRATYLETLSVTTKGFASALVPKVMKGVSVIBELDTSYCIETDLYCTRIVTFPMSP 240
QY 358 GIYSCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
DB 241 GIYSCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
QY 418 LIDRQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNA 477
DB 301 LIDRQSCNVLSLDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNA 360
QY 478 LDKLEESNKLKDVNKLKTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 537
DB 361 LDKLEESNKLKDVNKLKTSALITYIVLTIVSLVCGILSLVACILMYKQKQAKOQKTL 420
QY 538 WLGNNTLQMRATTKM 553
DB 421 WLGNNTLQMRATTKM 436

RESULT 3

US-10-267-748-94
Sequence 94, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.

Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatenIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-267-748-94
Query Match 75.7%; Score 2086.5; DB 12; Length 436;
Best Local Similarity 96.6%; Pred. No. 4.3e-172;
Matches 421; Conservative 2; Mismatches 12; Indels 1; Gaps 1;
QY 118 IGAIIGGAALGVATAAQITTAASALIQANONNANTILRKERIAATNEAVHEVTDGLSOLAV 177
DB 2 IGAIIGSVALGVATAAQITTAASALIQANONNANTILRKESITATIEAVHEVTDGLSOLAV 61
QY 178 AVGRMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALFQLTIOA 237
DB 62 AVGRMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETTVFGPQITSPALFQLTIOA 121
QY 238 LYNLAGNMDDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLQVTLPSVGNLNN 297
DB 122 LYN-AGNMDDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLGLQVTLPSVGNLNN 180
QY 298 MRATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIYTFPMSP 357
DB 181 MRATYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIYTFPMSP 240
QY 358 GIYCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 417
DB 241 GIYCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVS 300
QY 418 LIDRQSCNVLSLDGTTILSLGFEFDATYQKNISICDSQVIVTGNLIDISTELGNVNNISNA 477
DB 301 LIDRQSCNVLSLDGTTILSLGFEFDATYQKNISILDSQVIVTGNLIDISTELGNVNNISNA 360
QY 478 LDKLEESNKLKQNVNKLTSALITYIVLTVISLVCGLSILVACYLAMYKQKQKQKTL 537

DB 361 LDKLEESNKLKQNVNKLTSALITYIVLTVISLVCGLSILVACYLAMYKQKQKQKTL 420
QY 538 WLGNNTLDQMRTTKM 553
DB 421 WLGNNTLDQMRTTKM 436
RESULT 4
US-09-951-061A-141
; Sequence 141, Application US/09951061A
; Publication No. US20030082204A1
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; APPLICANT: Gettig, Russell
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell, Boehnen, Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/951,061A
; FILING DATE: 13-SEP-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/354,138
; FILING DATE: 15-JUL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,657
; FILING DATE: 16-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,962
; FILING DATE: 08-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776,867
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,614
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,283
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,483
; FILING DATE: 12-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/713,967
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07,666,056
; FILING DATE: 07-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2860

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: internal
US-09-951-061A-141

Query Match 22.6%; Score 623.5; DB 10; Length 662;
Best Local Similarity 27.3%; Pred. No. 6.4e-45;
Matches 143; Conservative 120; Mismatches 249; Indels 11; Gaps 5;
QY 19 VALALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSSTGSIIVKLLPNMPKDEACAK 78
Db 124 LGMASFLCSKAQIHWNNLSITIGITDVSVHYKIMTRPSHQVLYIKLMPVSL-TENCTK 182
QY 79 APLEAYNRTLTTLTPLGDSIRRIQESV-----TTSGGKGQRLGALIGAGALGVATAAQ 134
Db 183 AELGEYKLLSVLEPINOALTMKNVKPQLSGSGRRQRRFAGVILAGVATAAQ 242
QY 135 ITAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAGKMQQFVNDQFNKTA 194
Db 243 ITAGIALHQSUNLNAQAIQSLRTSLQSNKAIEETREATQETVIAVQGVQDYVNNELVPAM 302
QY 195 QELDCIKITQGVGVELNLYLTETLTFVFGPQITSPALTOITQALYNLAGNMVLLTKLG 254
Db 303 QHMSCELVGQRLGLRLRYTTELLSIFGPSLRDPISABISIQALIYALGGEIHKILKLG 362
QY 255 VGNQLSLSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATVLETLSVSTTKGF 314
Db 363 YSGDMTAILSRGKTKITHVDLPKFIILSYPTLSEVKGVIHVRLEAVSNIGSQE 422
QY 315 ASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYCLSGNTSACMYSK 374
Db 423 WYTTVPRIATNGVLIISNFDSESCVFSVSESAICSONSLYPSLPQQCIRGDTSCARTL 482
QY 375 TEGALTTPYMTLKSIVIANCMWTCRCADPPGIISQNYGEAVSLDRQSCNVLSDGHTL 434
Db 483 VSGTMGNKFIILSKGNIVANCASILCKCVSTSTIINQSPDKLLTFIASDTCPLVEIDGATI 542
QY 435 RLSGEF--DATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDKLEESNKLKVN 492
Db 543 QVGRQVPMVYEGKVAL--GPAISLDRLDVGTNGLNALKKDDAKVLDSSNQILETVR 600
QY 493 VKLTSTSAITYIVLTVISLVCGILSLVLACLYMYKQKQOKT 535
Db 601 RSSFNFGSLLSVPLSCTAL--ALLLLIYCKRRYQOTLKQHT 641

RESULT 5

US-10-670-695-36
; Sequence 36, Application US/10670695
; Publication No. US20040058316A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Wayne A.
; APPLICANT: Lappin, Michael R.
; APPLICANT: Rosen, David K.
; APPLICANT: Andrews, Janet S.
; TITLE OF INVENTION: USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE
; FILE REFERENCE: DI-9-1
; CURRENT APPLICATION NUMBER: US/10/670,695
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 09/521,738
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36

; LENGTH: 662
; TYPE: PRT
; ORGANISM: canine distemper virus
US-10-670-695-36

Query Match 22.5%; Score 621.5; DB 12; Length 662;
Best Local Similarity 27.3%; Pred. No. 9.6e-45;
Matches 143; Conservative 120; Mismatches 249; Indels 11; Gaps 5;
QY 19 VALALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSSTGSIIVKLLPNMPKDEACAK 78
Db 124 LGMASFLCSKAQIHWNNLSITIGITDVSVHYKIMTRPSHQVLYIKLIPNASL-TENCTK 182
QY 79 APLEAYNRTLTTLTPLGDSIRRIQESV-----TTSGGKGQRLGALIGAGALGVATAAQ 134
Db 183 AELGEYKLLSVLEPINOALTMKNVKPQLSGSGRRQRRFAGVILAGVATAAQ 242
QY 135 ITAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAGKMQQFVNDQFNKTA 194
Db 243 ITAGIALHQSUNLNAQAIQSLRTSLQSNKAIEETREATQETVIAVQGVQDYVNNELVPAM 302
QY 195 QELDCIKITQGVGVELNLYLTETLTFVFGPQITSPALTOITQALYNLAGNMVLLTKLG 254
Db 303 QHMSCELVGQRLGLRLRYTTELLSIFGPSLRDPISABISIQALIYALGGEIHKILKLG 362
QY 255 VGNQLSLSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATVLETLSVSTTKGF 314
Db 363 YSGDMTAILSRGKTKITHVDLPKFIILSYPTLSEVKGVIHVRLEAVSNIGSQE 422
QY 315 ASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYCLSGNTSACMYSK 374
Db 423 WYTTVPRIATNGVLIISNFDSESCVFSVSESAICSONSLYPSLPQQCIRGDTSCARTL 482
QY 375 TEGALTTPYMTLKSIVIANCMWTCRCADPPGIISQNYGEAVSLDRQSCNVLSDGHTL 434
Db 483 VSGTMGNKFIILSKGNIVANCASILCKCVSTSTIINQSPDKLLTFIASDTCPLVEIDGATI 542
QY 435 RLSGEF--DATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDKLEESNKLKVN 492
Db 543 QVGRQVPMVYEGKVAL--GPAISLDRLDVGTNGLNALKKDDAKVLDSSNQILETVR 600
QY 493 VKLTSTSAITYIVLTVISLVCGILSLVLACLYMYKQKQOKT 535
Db 601 RSSFNFGSLLSVPLSCTAL--ALLLLIYCKRRYQOTLKQHT 641

RESULT 6

US-09-873-233A-20
; Sequence 20, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
; FILE REFERENCE: 0216-0451P
; CURRENT APPLICATION NUMBER: US/09/873,233A
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(550)
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-873-233A-20

Query Match 22.0%; Score 606.5; DB 9; Length 550;
Best Local Similarity 28.2%; Pred. No. 1.4e-43;
Matches 148; Conservative 118; Mismatches 245; Indels 13; Gaps 7;

QY 17 VRVALASCVCPTSSLDGRPLAAGIVVTGKAVNIYTSQTGSIIVKLLPNMPKKEAC 76
DB 10 ILMAVLLTLQTPGTQIHGWSLKGIVGIGSASVKWTRSSHQSLVTKLMPNITL-LNNC 68
QY 77 AKAPLEAYNRTLLTLLPLGDSIRRIQESV-----TTSGGKGQGLGALGALGATA 132
DB 69 TRVEIAEYRLLRTVLEPIRDALNMTQNIIRPVQSVAASSRRHRKRFAGVWLAGAALGATA 128
QY 133 AQITAAASALIQAQNAANILRLKERIAATNEAVHEVTDLGSLAVAVGKMQQFVNDQFNK 192
DB 129 AQITAGIALHQSMLNSQALDNLRLASLETNQATEAIRQAGOEMLAVQGVQDIYNELIP 188
QY 193 TAGELDCIKITQOVGVBEINLYLTETTVFGPOITSPALQTOLTIQALYNLAGNMDYLLTK 252
DB 189 SMNQLSCDLIGQKGLKRLRYYTEILSLFGPSLRDPTSAEISIQALSVALGGDINKVLEK 248
QY 253 LGVGNNOISLISGLITGNPILYDSQTLGLIGQVTLPSVGNLNNMREATVLETLSVSTTK 312
DB 249 LGVSGDGLLGLESRGIKARITHVDTESYFIVLSIAYPTLSBIKGVIVHRLGVSNIGS 308
QY 313 GFASALYKVMKGVSVIEELDTSCYIETDLDTCTRIYVTFPMPSPGIYSCLSGNTSACMY 372
DB 309 QEWTTVPKYVATOGYILSNFDESSCTFMEPGTVCSQNALYPMSPLQECCLRGSTKSCAR 368
QY 373 SKTEGALTTPYMTLUGSVIANCKMTTCRCADPPGIIISQNGEAVSLIDROSQNVLSLDGI 432
DB 369 TLVSGSGFNRFILSQGNLIANCASILCKCTYTTGTIINQDPDKILTYIAADHCPVVEVNG 428
QY 433 TLRLSGEF--DATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDKLEESNKLDK 490
DB 429 TIQVGSRRYPDAVYLHRIDL--GPPISLERLDVGTNLGNIAKLEDAKELLESSDQILRS 486
QY 491 VNVKLTSTALITYIVLTV--ISLVCGLISLVLACVLMYKQKAAQ 533
DB 487 MK-GLSSTS--IVYLLIAVCLGLIGIPALICCCRCGRNKGEO 527
RESULT 7
US-09-873-233A-18
; Sequence 18, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
; FILE REFERENCE: 0216-0451P
; CURRENT APPLICATION NUMBER: US/09/873,233A
; CURRENT FILING DATE: 2001-06-05
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 550
; TYPE: PRF
; ORGANISM: Measles virus
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(550)
; OTHER INFORMATION: any n or xaa = Unknown
US-09-873-233A-18
Query Match 22.0%; Score 605.5; DB 9; Length 550;
Best Local Similarity 28.5%; Pred. No. 1.8e-43;
Matches 149; Conservative 116; Mismatches 244; Indels 13; Gaps 7;
QY 19 VALAISCVCPTSSLDGRPLAAGIVVTGKAVNIYTSQTGSIIVKLLPNMPKKEAC 78
DB 12 MAVLLTLQTPGTQIHGWSLKGIVGIGSASVKWTRSSHSHSLVTKLMPNITL-LNNCTR 70
QY 79 APLEAYNRTLLTLLPLGDSIRRIQESV-----TTSGGKGQGLGALGALGATAAQ 134
DB 71 VEIAEYRLLRTVLEPIRDALNMTQNIIRPVQSVAASSRRHRKRFAGVWLAGAALGATAAQ 130

QY 135 ITAASALIQAQNAANILRLKERIAATNEAVHEVTDLGSLAVAVGKMQQFVNDQFNKTA 194
DB 131 ITAGIALHQSMLNSQALDNLRLASLETNQATEAIRQAGOEMLAVQGVQDIYNELIPSM 190
QY 195 QELDCIKITQOVGVBEINLYLTETTVFGPOITSPALQTOLTIQALYNLAGNMDYLLTKLG 254
DB 191 NQUSCDLIGQKGLKRLRYYTEILSLFGPSLRDPTSAEISIQALSVALGGDINKVLEKLG 250
QY 255 VGNQNLSSLISGLITGNPILYDSQTLGLIGQVTLPSVGNLNNMREATVLETLSVSTTKGF 314
DB 251 YSGDGLLGLESRGIKARITHVDTESYFIVLSIAYPTLSBIKGVIVHRLGVSNIGSQE 310
QY 315 ASALYKVMKGVSVIEELDTSCYIETDLDTCTRIYVTFPMPSPGIYSCLSGNTSACMYSK 374
DB 311 WYTTVPKYVATOGYILSNFDESSCTFMEPGTVCSQNALYPMSPLQECCLRGFTKSCARTL 370
QY 375 TEGALTTPYMTLUGSVIANCKMTTCRCADPPGIIISQNGEAVSLIDROSQNVLSLDGITL 434
DB 371 VSGSGFNRFILSQGNLIANCASILCKCTYTTGTIINQDPDKILTYIADHCPVVEVNGVTI 430
QY 435 RLSGEF--DATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDKLEESNKLDKVN 492
DB 431 QVGSRRYPDAVYLHRIDL--GPPISLERLDVGTNLGNIAKLEDAKELLESSDQILRSKM 488
QY 493 VKLTSTALITYIVLTV--ISLVCGLISLVLACVLMYKQKAAQ 533
DB 489 -GLSSTS--IVYLLIAVCLGLIGIPALICCCRCGRNKGEO 527
RESULT 8
US-10-267-682-93
; Sequence 93, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Wild, Carl T.
; Matthews, Thomas J.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-3741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 93:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 438 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 93:
 US-10-267-748-93

```

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 93:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 438 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-267-748-93

Query Match          19.4%; Score 534; DB 12; Length 438;
Best Local Similarity 28.2%; Pred. No. 2e-37;
Matches 118; Conservative 97; Mismatches 198; Indels 6; Gaps 3

QY      119  CAITGGGAALGVATAAQTASALIQANQNNAANILRLKERIATNEAVHVTVDGLSQLAVA 178
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3    GVLAGVALGVATAAQTAGIALHQSLNNAQAQISLRTLEQSKAIEIREATQETVIA 62

QY      179  VGKMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTLTVRGPOITSPALTQTIOAL 238
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      53  VQGVQDYVNNELVPAMQHMSCSELVGRGLRGLRLRYITELLISFGPELRDPISAETISQAL 122

QY      239  YNLAGGNNQVLLTKLGVGNQLSSLGSLGTGNPIYDSQTQLLGIVTLPSVGNLNMN 298
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      123  IYALGGBIHKILEKGLGVSGSDMTAILESRGIKTKITHVDLPCKFIILSISYPTLSEVKGV 182

QY      299  RATYLETLSSVTTKGFASALVPKVMKVGSVLEELDTSYCIETDLDLYCTRVITVTPMSPG 358
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

359 IYSCLSGNTSACMYKTEGALITTPYMLTKGSVIANCKMTTCBAPPGIISQNYGEAVSL 418
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
dbb : : : : : : : : : : : : : : : : : : : : : : : : : : : :
243 LQCCIRGDTSSCARTLVSGTMGNKFTLSKGNIVANCA SILCKRCYSTSTIINQSPDKLTF 302
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
dbb : : : : : : : : : : : : : : : : : : : : : : : : : : : :
419 IDROSCNVLSDGTLRLSGEF--DATYOKNIISQDSQVIVTGNLIDISTELGNVNNISIN 476
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
dbb : : : : : : : : : : : : : : : : : : : : : : : : : : : :
303 IASDTCPLEVIDAATQVGRQDPMVYEGKVAL--GPAISLDRJLDVGTNLGNALKKLUDD 360
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
dbb : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 ALDKLEESNKLKDNVKLTSTISALITYIVLTVISLVCIGILSLVLACVLMYKQAQOQT 535
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
dbb : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 AKVLIDSSNQILETVRRSFNGSLSLVPLSCTAL--ALLLLIYCCRRYQOOLKQHT 417
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10
 US-10-267-682-105
 ; Sequence 105, Application US/10267682
 ; Publication No. US2004003235A1
 ; GENERAL INFORMATION:
 APPLICANT: Boicognesi, Dani P.
 Matthews, Thomas J.
 Wild, Carl T.
 Batney, Shawn O.
 Lambert, Dennis M.
 Petteway, Stephen R.
 Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-682-105

Query Match 18.3%; Score 504; DB 12; Length 438;
Best Local Similarity 29.7%; Pred. No. 7.8e-35;
Matches 124; Conservative 91; Mismatches 195; Indels 8; Gaps 5;
QY 119 GAIIGAGALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVEHVTGSLQSLAVA 178
DB 3 GVVLAGAGALGVATAAQTAGIALHQSLNMQADNLRLASLETNQAEARQAGQEMILA 62
QY 179 VGRMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALQTQAL 238
DB 63 VQGVQDYINNELIPSMNQSLDLIGQKLGKLLRYTTEILSLFGPSLRDPISAEISQAL 122
QY 239 YNLAGNMVLLTKLGVGNQSLSLGSLITGNPILYDSQTQLLGHQVTLPSVGNLNM 298
DB 123 SYALGGDINKVLEKLGSGGDLGILSRGKARITHVDTESYFIVLSIAYPTLSEIKGV 182
QY 299 RATVLETLVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLYCTRVTFPMSPG 358
DB 183 IVHRELVGSYINSGQEWYTPVKVATQGVLIISNFDSECTFMPEGVCQNALYPMSP 242
QY 359 IYSLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKVTCRCADPPGIISQNYGEAVSL 418
DB 243 LQECIRGSKSCARTLVSGSGFGRFILSQGNLIANCASILCKCYTTGTTINQDPDKILTY 302
QY 419 IDRQSCNVSLDGLTLRLSGEF--DATYQKNISIQDSQVIVTGNLDISTELGNVNNISN 476
DB 303 IAAHCPVVEVNGVTIQVGSRRYPDAVYLHRLDL--GPPISLERLDVGTNLGNIAKLED 360
QY 477 ALDKLEESNKLKDVNKLTSALITVIVTLV--ISLVCGILSLVLAACYLMYKQAKQ 533
DB 361 AKELLESQDLRLSMK--GLSSTS--IVYILIAVCLGLGILGIPALICCRGCRKKGQ 415

RESULT 11
US-10-267-748-105
; Sequence 105, Application US/10267748
; Publication No. US20040052820A1

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Peteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-748-105

Query Match 18.3%; Score 504; DB 12; Length 438;
Best Local Similarity 29.7%; Pred. No. 7.8e-35;
Matches 124; Conservative 91; Mismatches 195; Indels 8; Gaps 5;
QY 119 GAIIGAGALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVEHVTGSLQSLAVA 178
DB 3 GVVLAGAGALGVATAAQTAGIALHQSLNMQADNLRLASLETNQAEARQAGQEMILA 62
QY 179 VGRMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLVFGPQITSPALQTQAL 238
DB 63 VQGVQDYINNELIPSMNQSLDLIGQKLGKLLRYTTEILSLFGPSLRDPISAEISQAL 122
QY 239 YNLAGNMVLLTKLGVGNQSLSLGSLITGNPILYDSQTQLLGHQVTLPSVGNLNM 298
DB 123 SYALGGDINKVLEKLGSGGDLGILSRGKARITHVDTESYFIVLSIAYPTLSEIKGV 182
QY 299 RATVLETLVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLYCTRVTFPMSPG 358
DB 183 IVHRELVGSYINSGQEWYTPVKVATQGVLIISNFDSECTFMPEGVCQNALYPMSP 242
QY 359 IYSLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKVTCRCADPPGIISQNYGEAVSL 418
DB 243 LQECIRGSKSCARTLVSGSGFGRFILSQGNLIANCASILCKCYTTGTTINQDPDKILTY 302

QY 419 IDRQCNVLSDGTLRLSGER--DATYQKNISIODSQVIVTGNLDISTELGNVNNSIN 476
DB 303 IADHCPCVVEVNGVITQVSRYPDAVYLRIDL--GPFISLERLDVGTNLGNATAGLED 360
QY 477 ALDKLEENSKLDKVNKLTSTSLITYIVLTV--ISLVCGILSLVLACYLMTYKQKAAQ 533
DB 361 AKELLESSDQILRSKM--GLSSTS--IVYILIAVCLGLGILGIPALICCCRCGRCKKEGQ 415

RESULT 12

US-10-267-682-95
; Sequence 95, Application US/10267682
; Publication No. US20040033235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Petteway, Dennis M.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 95:

US-10-267-682-95

Query Match 16.6%; Score 458; DB 12; Length 430;
Best Local Similarity 27.6%; Pred. No. 7,4e-31;
Matches 118; Conservative 81; Mismatches 219; Indels 10; Gaps 1;
QY 119 GAITGGAALGVATAQITTAASALIQANQANILRLKERIAATNEAVHEVTDGLSQLAVA 178
DB 3 GGVICTIALGVATSAQITAAVAALVEAKQARSIEKLKEAIRDTNKAQVQSSIGNLIVA 62
QY 179 VGKMQQVNDQFNKTAQELDCIKITQQGVNELNLYLTITVFGPQITSPALTOITQAL 238
DB 63 IKSVDQYVKNKEIVPSIARLGEAGLQIGIALTOHYSELTNIFGDNIGLSQEKGLQGI 122

RESULT 13

US-10-267-748-95

; Sequence 95, Application US/10267748

; Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Petteway, Dennis M.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: amino acid

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRVA.....KTLMLGNNTDQMRATMM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1:	Geneseqp19808:*
2:	Geneseqp19908:*
3:	Geneseqp20008:*
4:	Geneseqp20018:*
5:	Geneseqp20028:*
6:	Geneseqp20038:*
7:	Geneseqp20038:*
8:	Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	2 AAR10065	Aar10065 Newcastle
2	2716	98.5	553	6 ABR56236	Abr56236 Newcastle
3	2620	95.0	1103	6 ABR39678	Abr39678 Amino aci
4	2616	94.9	553	3 AAY51231	Aay51231 Newcastle
5	2610	94.7	553	2 AAR58858	Aar58858 Newcastle
6	2610	94.7	553	2 AAR49141	Aar49141 Newcastle
7	2610	94.7	553	2 AAW06828	Aaw06828 Newcastle
8	2610	94.7	553	2 AAR10691	Aar10691 Newcastle
9	2610	94.7	553	2 AAY21983	Aay21983 Seq ID No
10	2610	94.7	553	3 AAB58183	Aab58183 NDV fusio
11	2610	94.7	553	3 AAB36039	Aab36039 Protein e
12	2606	94.5	553	2 AAR14480	Aar14480 Newcastle
13	2606	94.5	553	2 AAW44941	Aaw44941 Newcastle
14	2603	94.4	553	1 AAP70176	Aap70176 Sequence
15	2493.5	90.4	564	5 ABG31709	Abg31709 Newcastle
16	2401	87.1	526	1 AAP80986	Aap80986 Sequence
17	2386	86.5	526	2 AAR20501	Aar20501 Newcastle
18	2086.5	75.7	436	6 ABO10250	Abo10250 Newcastle
19	2065	74.9	437	4 AAU14030	Aau14030 Peptide s
20	717	26.0	529	6 ABJ18515	Abj18515 Human Cry
21	715	25.9	529	6 ABJ18516	Abj18516 Canine pa
22	714	25.9	551	6 ABJ18506	Abj18506 Human Cry
23	712	25.8	551	6 ABJ18514	Abj18514 Simian vi
24	707	25.6	551	6 ABJ18513	Abj18513 Simian vi
25	706	25.6	529	4 ABP98712	Abp98712 Canine pa

26	696.5	25.3	532	6	ABJ18507	Abj18507 Human Cry
27	694.5	25.2	538	4	AA67476	Aab67476 Amino aci
28	689	25.0	542	2	AAR24076	Aar24076 Para-infl
29	623.5	22.6	662	2	AAR83304	Aar83304 Canine di
30	623.5	22.6	662	5	AA47653	Aam47653 Canine di
31	621.5	22.5	662	3	AA08102	Aam08102 Amino aci
32	621.5	22.5	662	3	AA08102	Aam08102 Amino aci
33	610.5	22.1	550	4	AAW50124	Aam50124 Canine di
34	610.5	22.1	550	4	AAW50124	Aam50124 Canine di
35	608.5	22.1	550	4	AAW50124	Aam50124 Canine di
36	606.5	22.0	550	2	AAW50124	Aam50124 Canine di
37	606.5	22.0	550	2	AAW50124	Aam50124 Canine di
38	606.5	22.0	550	2	AAW50124	Aam50124 Canine di
39	605.5	22.0	550	2	AAW50124	Aam50124 Canine di
40	605.5	22.0	550	4	AAW50124	Aam50124 Canine di
41	602.5	21.9	550	2	AAW50124	Aam50124 Canine di
42	590.5	21.4	449	6	ABJ18509	Abj18509 Human Cry
43	552	20.0	539	2	AB39283	Aar39283 Parainflu
44	534	19.4	438	6	ABO10249	Abo10249 Canine di
45	522.5	19.0	439	4	AAU14029	Aau14029 Peptide s

ALIGNMENTS

RESULT 1
AAR10065
ID AAR10065 standard; protein; 553 AA.
XX
AC AAR10065;
XX
DT 25-MAR-2003 (revised)
DT 14-MAR-1991 (first entry)
XX
DE Newcastle disease virus (NDV) F gene product.
XX
KW Avipoxvirus; fowlpoxvirus; vaccine.
XX
OS Newcastle disease virus.
XX
PN EP404576-A.
XX
PD 27-DEC-1990.
XX
PF 21-JUN-1990; 90EP-00306806.
XX
PR 22-JUN-1989; 89JP-00160157.
XX
PA (JAPG) NIPPON ZEON KK.
PA (SHIO) SHIONOGI & CO LTD.
PA (YANA/) YANAGIDA N.
XX
PI Yangida N, Saeki S, Okawa S, Kmanogawa K, Iritani Y, Sawaguchi K;
XX WPI: 1991-001591/01.
XX N-PSDB; AAQ10060.
XX
PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus
PT in region non-essential for proliferation, used as live vaccine in fowls.
XX
PS Claim 3; Fig 3; 23pp; English.
XX
CC The sequence encoding the protein may be incorporated into a recombinant
CC Avipoxvirus and used as a live vaccine in fowls, providing immunity to
CC fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 553 AA;

Query Match 98.8%; Score 2724; DB 2; Length 553;
Best Local Similarity 98.4%; Pred. NO. 9.8e-226;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSVCPTSSLDGRPLAAGIVTGDKAIVNITSSQTGS 60

```

Db      1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
QY      61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120
Db      61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120
QY      121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQSLAVAG 180
Db      121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQSLAVAG 180
QY      181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240
Db      181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240
QY      241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db      241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY      301 TYLETLSVSTTKGFASALVPKVVMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 360
Db      301 TYLETLSVSTTKGFASALVPKVVMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 360
QY      361 SCLSGNTSACWYSKTEGALTTPYMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db      361 SCLSGNTSACWYSKTEGALTTPYMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY      421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db      421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
QY      481 LEESNKLKDVNKLSTSAITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG 540
Db      481 LEESNKLKDVNKLSTSAITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG 540
QY      541 NNTLDQMRATTKM 553
Db      541 NNTLDQMRATTKM 553

```

RESULT 2

ABR56236
ID ABR56236 standard; protein; 553 AA.

XX ABR56236;

XX 20-NOV-2003 (first entry)

XX Newcastle disease virus (NDV) Fusion (F)-protein.

XX F-protein; virucide; vaccine; anti-viral; Fusion protein;

XX protein co-ordinate data.

XX Newcastle disease virus.

XX WO2003040178-A1.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-AU001522.

XX 09-NOV-2001; 2001AU-00008784.

XX (BIOT-) BIOTA HOLDINGS LTD.

XX Morton CJ, Parker MW, Ryan J;

XX WPI; 2003-441524/41.

XX Identifying, screening or modifying anti-viral agents, by generating a 3-dimensional structure model of respiratory Syncytial virus-F protein having a target site to interact with an anti-viral agent that inhibit RSV-F.

XX

PS Disclosure; Fig 1; 224pp; English.

XX

CC The present invention relates to a method (M1) for identifying a candidate anti-viral agent (I), screening compounds and/or chemical complexes for (I), modifying (I) to improve anti-viral activity, or producing anti-viral agents, by generating a 3-dimensional structure model of Respiratory Syncytial virus (RSV) Fusion (F)-protein with 3-dimensional structure of target site to which an anti-viral agent may interact and thus inhibit RSV-F protein activity. The present sequence is the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment with the RSV F-protein sequence (ABR56234)

XX Sequence 553 AA;

QY Query Match 98.5%; Score 2716; DB 6; Length 553;
Best Local Similarity 98.2%; Pred. No. 4.8e-225;
Matches 543; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

Db 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120

Db 61 IIVKLLPNMPKDEKACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRILGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQSLAVAG 180

Db 121 IIGGAALGVATAAQITAAASALIQANQANILRLKESIAATNEAVHEVTGSLQSLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240

Db 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTIQALYN 240

QY 241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

Db 241 LAGNNMDYLLTKLGVGNQLSSLTGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVVMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 360

Db 301 TYLETLSVSTTKGFASALVPKVVMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 360

QY 361 SCLSGNTSACWYSKTEGALTTPYMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 420

Db 361 SCLSGNTSACWYSKTEGALTTPYMTLXGSIANCKMTTCRCADPPGIISQNYGEAVSLID 420

QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480

Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480

QY 481 LEESNKLKDVNKLSTSAITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG 540

Db 481 LEESNKLKDVNKLSTSAITYIVLTIVSLVCGILSLVACVLMYKQKQAQKTLWLIG 540

QY 541 NNTLDQMRATTKM 553

Db 541 NNTLDQMRATTKM 553

RESULT 3

ABR39678

ID ABR39678 standard; protein; 1103 AA.

XX ABR39678;

XX 23-JUN-2003 (first entry)

XX Amino acid sequence of F protein and partial HN protein.

XX NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;
KW haemagglutinin-neuraminidase; cytostatic; gene therapy; cancer.
XX

QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 QY 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 DB 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
 DB 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
 QY 481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACVLMYKOKAQKTLMLWG 540
 DB 481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACVLMYKOKAQKTLMLWG 540
 QY 541 NNTLDQMRATTKM 553
 DB 541 NNTLDQMRATTKM 553

RESULT 2

A46329
 Cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
 N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
 C;Species: Newcastle disease virus
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A46329
 R;Royoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
 Virology 169, 273-282, 1989
 A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
 A;Reference number: A46329; MUID:99204898; PMID:2705298
 A;Accession: A46329
 A;Molecule type: Genomic RNA
 A;Residues: 1-553 <TOY>
 A;Cross-references: GB:M24692; NID:g293919; PIDN:AAA46643.1; PID:g293920
 C;Genetics:
 A;Gene: F
 C;Superfamily: parainfluenza virus cell fusion protein

Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 98.4%; Pred. No. 1.4e-162;
 Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 DB 1 MGSRSSTRIPVPLMLTVRIMALUSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 DB 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240

Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 98.4%; Pred. No. 1.4e-162;
 Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 DB 1 MGSRSSTRIPVPLMLTVRIMALUSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 DB 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240

QY 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 DB 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
 DB 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
 QY 481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACVLMYKOKAQKTLMLWG 540
 DB 481 LEESNSKLDKVNKLTSTLSALITVIVTSLVCGILSLVACVLMYKOKAQKTLMLWG 540
 QY 541 NNTLDQMRATTKM 553
 DB 541 NNTLDQMRATTKM 553

RESULT 3

S23621
 Gene F protein - Newcastle disease virus
 C;Species: Newcastle disease virus
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
 C;Accession: S23621
 R;Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
 Virus Res. 15, 237-242, 1990
 A;Title: A host range mutant of Newcastle disease virus with an altered cleavage site f
 A;Reference number: S23620; MUID:90261333; PMID:2188464
 A;Accession: S23621
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-553 <PRI>
 A;Cross-references: EMBL:Z12110
 C;Superfamily: parainfluenza virus cell fusion protein

Query Match 97.6%; Score 2691; DB 2; Length 553;
 Best Local Similarity 98.2%; Pred. No. 1.7e-160;
 Matches 543; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 DB 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
 DB 121 IIGGALGVATAAQITAAASALIOANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKITQQVGVELNLYLTTLTTFVGPQITSPALQTQIALYN 240
 QY 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 DB 241 LAGNMNDYLLTKLGVGNQSLSSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2
Perfect score: 2757
Sequence: 1 MGRSRSTRIPVPLMLTVRVA.....KTLMLGNNTLDQMRRATTK 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues 283366
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion glycop
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 G46329	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 E46329	cell fusion glycop
17	2585	93.8	553	1 E46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23620	gene F protein - N
21	2554	92.6	553	2 S23620	gene F protein - N
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZNM	cell fusion glycop
26	712.5	25.8	538	2 S52472	cell fusion glycop
27	704	25.5	538	1 VGNZMS	cell fusion glycop
28	704	25.5	551	1 VGNZFP	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZU1

cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/6 N; Contains: fusion glycoprotein F1; fusion glycoprotein F2
C; Species: Newcastle disease virus
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C; Accession: A29823, C46329
R; Millar, N.S.; Chambers, P.; Emerson, P.T.
J. Gen. Virol. 69, 613-620, 1988
A; Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoproteins.

A; Reference number: A92799; UID:88171450; PMID:3351479

A; Accession: A29823

A; Molecule type: mRNA

A; Residues: 1-553 <ML>

A; Cross-references: GB:D00243; NID:G222174; PIDN:BAA00173.1; PID:G222175

A; Experimental source: strain Ulster

R; Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y. Virology 169, 273-282, 1989

A; Title: Newcastle disease virus evolution. II. Lack of gene recombination in generation

A; Reference number: A46329; UID:89204898; PMID:2705298

A; Accession: C46329

A; Molecule type: Genomic RNA

A; Residues: 1-553 <TOY>

A; Cross-references: GB:M24694; NID:G293923; PIDN:AAA46645.1; PID:G293924

A; Experimental source: strain ULS/67

C; Genetics:

A; Gene: F

C; Superfamily: parainfluenza virus cell fusion protein

C; Keywords: glycoprotein; membrane fusion; transmembrane protein

F; 1-25/Domain: signal sequence #status predicted <SIG>

F; 26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F; 118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>

F; 495-528/Domain: transmembrane #status predicted <TM>

F; 85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;

Best Local Similarity 99.1%; Pred. No. 1.4e-162;

Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRSRSTRIPVPLMLTVRVALSCVPTSSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

|||||

Db 1 MGRSRSTRIPVPLMLTVRVALSCVPTSSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

|||||

Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

|||||

Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

|||||

Qy 121 IIGGALGVATAAQITTAASALIQANQNAANILRLK AATNEAVHEVTDGLSQLAVAG 180

|||||

Db 121 IIGGALGVATAAQITTAASALIQANQNAANILRLK AATNEAVHEVTDGLSQLAVAG 180

|||||

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OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 40 Seconds
(without alignments)
719.870 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGRSRSTRIPVPLMLTVRA.....KTLMLGNLTLDQMRATYK 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	1	VGLF_NDND
2	2724	98.8	553	1	VGLF_NDVU
3	2684	97.4	553	1	VGLF_NDVQ
4	2622	95.1	553	1	VGLF_NDVH4
5	2618	95.0	553	1	VGLF_NDVA
6	2606	94.5	553	1	VGLF_NDVT
7	2603	94.4	553	1	VGLF_NDVB
8	2598	94.2	553	1	VGLF_NDVH3
9	2593	94.1	553	1	VGLF_NDVTH
10	2588	93.9	553	1	VGLF_NDVI
11	2588	93.9	553	1	VGLF_NDVL
12	2579	93.5	553	1	VGLF_NDVM
13	717	26.0	529	1	VGLF_SV5
14	712.5	25.8	538	1	VGLF_MUMPM
15	706	25.6	551	1	VGLF_P12H
16	704	25.5	538	1	VGLF_MUMPL
17	704	25.5	551	1	VGLF_P12HT
18	701.5	25.4	538	1	VGLF_MUMPR
19	701	25.4	551	1	VGLF_P12HG
20	691	25.1	538	1	VGLF_MUMPS
21	691	25.1	538	1	VGLF_SV41
22	636	23.1	631	1	VGLF_PHODV
23	631	22.9	546	1	VGLF_RINDS
24	621.5	22.5	662	1	VGLF_CDOV
25	610.5	22.1	550	1	VGLF_MEASA
26	608.5	22.1	546	1	VGLF_RINDL
27	605.5	22.0	550	1	VGLF_MEASE
28	603.5	21.9	546	1	VGLF_RINDK
29	599.5	21.7	546	1	VGLF_RINDR
30	590.5	21.4	534	1	VGLF_MEASV
31	581.5	21.1	529	1	VGLF_MEASI
32	546.5	19.8	539	1	VGLF_P13H4
33	521	18.9	565	1	VGLF_SENDJ

RESULT 1

ID	VGLF_NDND	STANDARD;	PRT;	553 AA.
AC	P35936;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Fusion glycoprotein precursor [Contains: Fusion glycoprotein P2;			
DE	Fusion glycoprotein F1]			
GN	F.			
OS	Newcastle disease virus (strain D26/76) (NDV).			
OC	Viruses; SRNA negative-strand viruses; Mononegavirales;			
OC	Paramyxoviridae; Paramyxovirinae; Rubulavirus.			
OX	NCBI_TaxID=11180;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8920498; PubMed=2705298;			
RA	Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,			
RA	Nagai Y.;			
RT	"Newcastle disease virus evolution. II. Lack of gene recombination in			
RT	generating virulent and avirulent strains.";			
RL	Virology 169:273-282(1989).			
CC	-!- FUNCTION: This protein directs fusion of viral and cellular			
CC	membranes.			
CC	-!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2			
CC	LINKED BY A DISULFIDE BOND.			
CC	-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein			
CC	family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; M24692; AAA46643.1; -			
DR	PIR; A46329; A46329.			
DR	PDB; 1GSG; 27-FEB-02.			
DR	InterPro; IPR000776; Fusion gly.			
DR	Pfam; PF00523; fusion gly; 1.			
KW	Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;			
KW	Lipoprotein; Palmitate; 3D-structure.			
FT	SIGNAL	1	25	
FT	CHAIN	26	553	FUSION GLYCOPROTEIN FO.
FT	CHAIN	26	116	F2 PROTEIN.
FT	CHAIN	117	553	F1 PROTEIN.
FT	TRANSMEM	117	136	POTENTIAL.
FT	DOMAIN	137	500	EXTRACELLULAR.
FT	TRANSMEM	501	527	POTENTIAL.
FT	DOMAIN	528	553	CYTOPLASMIC.
FT	CARBOHYD	85	85	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	191	191	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	366	366	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	447	447	N-LINKED (GLCNAC. . .) (POTENTIAL).

P12575 sendai viru
P09990 bovine para
P04855 sendai viru
P12605 human para
P04856 sendai viru
P13843 human respi
P03420 human respi
P11209 human respi
P12568 human respi
P23728 bovine respi
P24614 turkey rhin
P29791 bovine respi

ALIGNMENTS

FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 523 523 S-palmitoyl cysteine (in host)
 FT (Potential)
 SQ SEQUENCE 553 AA; 58892 MW; B90AA98D77CCC470 CRC64;
 Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 98.4%; Pred. No. 2.5e-162;
 Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS 60
 Db 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS 60
 Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 Qy 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 Db 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
 Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
 Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
 Qy 241 LAGGNMDDLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGGNMDDLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Qy 361 SCLSGNTSACMYSTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMYSTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Qy 421 ROSCNVLSDGTLRLSGEPDATYKNIISODSVIVTGNLIDISTELGNVANSISNALDK 480
 Db 421 ROSCNVLSDGTLRLSGEPDATYKNIISODSVIVTGNLIDISTELGNVANSISNALDK 480
 Qy 481 LEESNKLKVNKLTSTALITYIVLTIVSLVCGILSLVLAICYMYKQAKQKTLMLWG 540
 Db 481 LEESNKLKVNKLTSTALITYIVLTIVSLVCGILSLVLAICYMYKQAKQKTLMLWG 540
 Qy 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKM 553

RESULT 2

VCLF_NDVU STANDARD; PRT; 553 AA.
 ID VCLF_NDVU AC
 AC P12570;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 Fusion glycoprotein F1].
 DE F.
 GN F.
 OS Newcastle disease virus (strain Ulster/67) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=3351479;
 RA Millar N.S., Chambers P., Emerson P.T.;
 RT "Nucleotide sequence of the fusion and haemagglutinin-neuraminidase
 glycoprotein genes of Newcastle disease virus, strain Ulster;
 RT molecular basis for variations in pathogenicity between strains.";
 RL J. Gen. Virol. 69:613-620(1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=2705298;
 RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. II. Lack of gene recombination in
 generating virulent and avirulent strains.";
 RL Virology 169:273-282(1989).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D00243; BAA00173.1; -;
 DR EMBL; M24694; AAA46645.1; -;
 DR PIR; A29823; VGNZU1.
 DR InterPro: IPR00076; Fusion gly.
 DR Pfam; PF00523; Fusion_gly; 1.
 DR Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 KW Lipoprotein; Palmitate.
 FT SIGNAL 1 25
 FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
 FT CHAIN 26 116 F2 PROTEIN.
 FT CHAIN 117 553 F1 PROTEIN.
 FT CHAIN 117 136 POTENTIAL.
 FT TRANSMEM 137 500 EXTRACELLULAR.
 FT DOMAIN 501 527 POTENTIAL.
 FT DOMAIN 528 553 CYTOPLASMIC.
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 523 523 S-palmitoyl cysteine (in host)
 FT LIPID 523 523 (Potential).
 FT
 SQ SEQUENCE 553 AA; 58682 MW; FC99C763D8E2F7FA CRC64;
 Query Match 98.8%; Score 2724; DB 1; Length 553;
 Best Local Similarity 99.1%; Pred. No. 2.5e-162;
 Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS 60
 Db 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTQGS 60
 Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQSVTSSGGKQRLIGA 120
 Qy 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 Db 121 IIGGAALGVATAAQTAAALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
 Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
 Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETVFGPQITSPALTIQALYN 240
 Qy 241 LAGGNMDDLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGGNMDDLTKLGVGNQLSSGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360


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QY 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRSADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSAITVIVTSLVCGILSLVACLYMYKQKQAQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITVIVTSLVCGILSLVACLYMYKQKQAQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 3
VGLF NDVQ
ID VGLF NDVQ STANDARD; PRT; 553 AA.
AC P33615;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Queensland/66) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL; M24693; AAA46644.1; ..
DR PIR; B46329; B46329.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host
FT SEQUENCE 553 AA; 58866 MW; 38144816A45B3EF7 CRC64;
Query Match 97.48; Score 2684; DB 1; Length 553;
Best Local Similarity 97.34; Pred. No. 7.7e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MGRSSSRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTGTS 60
Db 1 MGRSSSRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSSTGTS 60
QY 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQANALILKESIAATNEAVEHTNGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQANALILKESIAATNEAVEHTNGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETTTVFGPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNLSSLISSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNRA 300
Db 241 LAGNMDYLLTKLGVGNQNLSSLISSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCVETDLDLYCTRTVTPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCVETDLDLYCTRTVTPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSAITVIVTSLVCGILSLVACLYMYKQKQAQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITVIVTSLVCGILSLVACLYMYKQKQAQKTLMLWG 540
QY 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 4
VGLF NDVH4
ID VGLF NDVH4 STANDARD; PRT; 553 AA.
AC P33613;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain B1-Hitchner/47) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11181;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular

```

membranes.
 -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 LINKED BY A DISULFIDE BOND.
 -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein family.

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 EMBL; M24695; AAA46646.1; -;
 PIR; D46329; D46329;
 InterPro; IPR000776; Fusion gly.
 Pfam; PF00523; fusion_gly; 1.
 Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 Lipoprotein; Palmitate.
 SIGNAL 1 25
 CHAIN 26 553 FUSION GLYCOPROTEIN FO.
 CHAIN 26 116 F2 PROTEIN.
 CHAIN 117 553 F1 PROTEIN.
 TRANSMEM 117 136 POTENTIAL.
 DOMAIN 137 500 EXTRACELLULAR.
 TRANSMEM 501 527 POTENTIAL.
 DOMAIN 528 553 CYTOPLASMIC.
 CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 LIPID 523 S-palmitoyl cysteine (in host) (Potential).
 SEQUENCE 553 AA; 58909 MW; F163E9B7CFDE4493 CRC64;
 Query Match 95.1%; Score 2622; DB 1; Length 553;
 Best Local Similarity 93.5%; Pred. No. 5.6e-156;
 Matches 517; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 1 MGRSSTRIPVPLMLTVRVALSVCPTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
 1 MGRSSTKIPAPMLTIRVALVLSICPANSIDGRPLAAGIVVTGDKAVNIYTSQTGS 60
 61 IIVKLLPNPKDKEACAPLEAYNRTLTLLTPLGDSIRRTQESVTTSGGKQRLIGA 120
 61 IIVKLLPNPKDKEACAPLDAYNRTLTLLTPLGDSIRRTQESVTTSGGKQRLIGA 120
 121 IIGGAALGVATAAQITTAASALIQANONANILRLKERTAAATNEAVHEVTDGLSOLAVAG 180
 121 IIGGVALGVATAAQITTAALIQANONANILRLKESAAATNEAVHEVTDGLSOLAVAG 180
 181 KMQFVNDQFNKTAQELDCIKITQGVNELNYLTETLTTFVFPQITSPALTTIQAALYN 240
 181 KMQFVNDQFNKTAQELDCIKIAQGVNELNYLTETLTTFVFPQITSPALNKITIQALYN 240
 241 LAGGNMDYLLTKLGVNNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 241 LAGGNMDYLLTKLGVNNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY 360
 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCTRTVTFPMSPGIY 360
 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVPPGIIISQNYGEAVSLID 420
 421 ROSCNVLSLDGTLRLSGFDATYOKNISQDSQVITVGNLIDISTELGVNNSISNALDK 480
 421 KOSCNVLSLGGITLRLSGFDFYOKNISQDSQVITVGNLIDISTELGVNNSISNALNK 480

QY 481 LEENSKLDKVNKLTSTSLITYTLVTLVTSILVCGILSLVACYLMYKQKQKQKTLWLG 540
 DB 481 LEENSKLDKVNKLTSTSLITYTLVTLVTSILVCGILSLVACYLMYKQKQKQKTLWLG 540
 QY 541 NNTLDQMRATTKM 553
 DB 541 NNTLDQMRATTKM 553
 RESULT 5
 VGLF NDVA
 ID VGLF NDVA STANDARD; PRT; 553 AA.
 AC P12572;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 Fusion glycoprotein F1].
 GN F.
 OS Newcastle disease virus (strain Australia-Victoria/32) (NDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OC NCBI TaxID=111177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89204898; PubMed=2705298;
 RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
 RA Nagai Y.;
 RT "Newcastle disease virus evolution. II. Lack of gene recombination in
 RT generating virulent and avirulent strains.";
 RL Virology 169:273-282(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87044526; PubMed=3776349;
 RA McGinnes L.W., Morrison T.G.;
 RT "Nucleotide sequence of the gene encoding the Newcastle disease virus
 RT fusion protein and comparisons of paramyxovirus fusion protein
 RT sequences.";
 RL Virus Res. 5:343-356(1986).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.

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 EMBL; M24700; AAA46650.1; -;
 EMBL; M21881; AAA46641.1; -;
 PIR; S07422; H46329.
 InterPro; IPR000776; Fusion gly.
 Pfam; PF00523; fusion_gly; 1.
 Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
 Lipoprotein; Palmitate.
 SIGNAL 1 25 FUSION GLYCOPROTEIN FO.
 CHAIN 26 553 F2 PROTEIN.
 CHAIN 26 116 F1 PROTEIN.
 CHAIN 117 553 POTENTIAL.
 TRANSMEM 117 136 EXTRACELLULAR.
 DOMAIN 137 500 POTENTIAL.
 TRANSMEM 501 527 CYTOPLASMIC.
 DOMAIN 528 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT LIPID 523 523 S-palmitoyl cysteine (in host)
FT FT (Potential)
FT CONFLICT 66 66 H -> L (IN REF. 2).
FT CONFLICT 162 162 I -> N (IN REF. 2).
SQ SEQUENCE 553 AA; 59022 MW; 0777BF9B6B1D1D27 CRC64;

Query Match 95.0%; Score 2618; DB 1; Length 553;
Best Local Similarity 95.3%; Pred. No. 9.9e-156;
Matches 52; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTGTS 60
DB 1 MGPSSSTRIPVPLMLTRIALALSCVHLASLSDGRPLAAAGIVVTGDKAVNIYTSSTGTS 60
QY 61 IIVKLLPNMPKDKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKGRLLGA 120
DB 61 IIVKLLPNMPKDKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKGRLLGA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITTAASALIQAQNAANILRLKESITATIEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTLLTPGPOITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTLLTPGPOITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLIGIQTLPVSGNLMNRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLIGIQTLPVSGNLMNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLNGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIHLRSLGSEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
DB 421 RHCNVSLDGIHLRSLGSEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480
QY 481 LBSNSKLDKVNKLTSTSLITVITVLSVCGILSLVLACVLMYKQAKQKTLWLWG 540
DB 481 LBSNSKLDKVNKLTSTSLITVITVLSVCGILSLVLACVLMYKQAKQKTLWLWG 540
QY 541 NNTLDQMRATTXM 553
DB 541 NNTLDQMRATTXM 553

RESULT 6
VGLF_NDVT STANDARD; PRT; 553 AA.
AC P26628;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Texas) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90204652; PubMed=2157037;
RA Taylor J., Edbauer C., Rey-Senelange A., Bouquet J.F., Norton E.,
RA Goebel S., Desmettre P., Paolletti E.;
RT "Newcastle disease virus fusion protein expressed in a fowlpox virus
recombinant confers protection in chickens.";

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J. Virol. 64:1441-1450 (1990).
-!- FUNCTION: This protein directs fusion of viral and cellular
membranes.
-!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.

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or send an email to license@isb-sib.ch).

EMBL; M33855; AAA46675.1; -.
PIR; A34663; VGNZTE.
InterPro; IPR000776; Fusion_gly.
Pfam; PF00523; Fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
FT SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
FT S-
SQ SEQUENCE 553 AA; 59042 MW; 4D335F8E159757B7 CRC64;

Query Match 94.5%; Score 2606; DB 1; Length 553;
Best Local Similarity 94.8%; Pred. No. 5.6e-155;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTGTS 60
DB 1 MGRSSTRIPVPLMLTIRALTALTSCLRLTSLDGRPLAAAGIVVTGDKAVNIYTSSTGTS 60
QY 61 IIVKLLPNMPKDKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKGRLLGA 120
DB 61 IIVKLLPNMPKDKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKGRLLGA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQITTAASALIQAQNAANILRLKESITATIEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTLLTPGPOITSPALTIQALYN 240
DB 181 KMQQFVNDQFNNTAQELDCIKITQOVGVNELNLYLTLLTPGPOITSPALTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLIGIQTLPVSGNLMNRA 300
DB 241 LAGGNMDYLLTKLGVGNQNLSSLIIGSLITGNPILYDSOTQLIGIQTLPVSGNLMNRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIHLRSLGSEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNSISNALDK 480

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Db 421 RHSCNVSLDGIITLRLSGEPDATYQKNISILDSQVIVTGNLDISTELGNVNNISNALNK 480
Qy 481 LEENSXKLDKVNKLTSTTSALITYIVLTVISLVCGLSLVACLYMYKQKQKQKTLMLG 540
Db 481 LEENSXKLDKVNKLTSTTSALITYIVLTVISLVCGLSLVACLYMYKQKQKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 7
VGLF NDVB
ID VGLF NDVB STANDARD; PRT; 553 AA.
AC P06156;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Beaudette C/45) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11178;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=87085486; PubMed=3025345;
RA Chambers P., Millar N.S., Emmerson P.T.;
RT "Nucleotide sequence of the gene encoding the fusion glycoprotein of
RT Newcastle disease virus.";
RL J. Gen. Virol. 67:2685-2694 (1986).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282 (1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC
CC -----
CC EMBL; X04719; CAA28426.1; -
CC EMBL; M24697; AAA46648.1; -
CC EMBL; A03663; AAA00288.1; -
CC F1R; A27008; VGNZNV.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion gly; 1.
CC Lipoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
CC Lipoprotein; Palmitate.
CC SIGNAL
CC 1 25
CC CHAIN 26 553 FUSION GLYCOPROTEIN F0.
CC CHAIN 26 116 F2 PROTEIN.
CC CHAIN 117 553 F1 PROTEIN.
CC CHAIN 117 136 POTENTIAL.
CC DOMAIN 137 500 EXTRACELLULAR.
CC TRANSMEM 501 527 POTENTIAL.
CC DOMAIN 528 553 CYTOPLASMIC.
CC CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
FT (Potential).
SQ SEQUENCE 553 AA; 59041 MW; 63BFD1692AFDE191 CRC64;

Query Match 94.4%; Score 2603; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 8.5e-155; Indels 0; Gaps 0;
Matches 517; Conservative 19; Mismatches 17;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVCPSTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
Db 1 MGRPSTYKXNPVPMMLTVRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
Qy 61 IIVKLLNPMKDKKACAKAPLEAVNRTLTLLTLPGLDSIRRIQESVTTSGGKGRLIGA 120
Db 61 IIVKLLNPLPKDKKACAKAPLDAYNRTLTLLTLPGLDSIRRIQESVTTSGGRQKRFIGA 120
Qy 121 IIGGALGVATAAQITAAASALIQAQNAANILRLKERTAAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGVALGVATAAQITAAALIQAKNAANILRLKESAAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVLEMLYLTELTVFQPQITSPALTIQALYN 240
Db 181 KMQOFVNDQFNKTAQELGCIIRIAQOVGVLEMLYLTELTVFQPQITSPALNKLTQALYN 240
Qy 241 LAGNMDYLLPKLGVGNQNLSSLGSLITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
Db 241 LAGNMDYLLPKLGVGNQNLSSLGSLITGNPILYDSOTQLGLQVTLPSVGNLNNRA 300
Qy 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCYTRIVTFPMSPGIY 360
Db 301 TYLETLVSSTTRGFASALVPKVTQVGSVIEBELDTSYCIETDLDLYCYTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID 420
Qy 421 RQSCNVSLDGIITLRLSGEPDATYQKNISIODSQVIVTGNLDISTELGNVNNISNALNK 480
Db 421 RQSCNVSLDGIITLRLSGEPDATYQKNISIODSQVIVTGNLDISTELGNVNNISNALNK 480
Qy 481 LEENSXKLDKVNKLTSTTSALITYIVLTVISLVCGLSLVACLYMYKQKQKQKTLMLG 540
Db 481 LEENSXKLDKVNKLTSTTSALITYIVLTVISLVCGLSLVACLYMYKQKQKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
```

RESULT 8

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VGLF NDVB
ID VGLF NDVB3 STANDARD; PRT; 553 AA.
AC P33612;
DT 01-PEB-1994 (Rel. 28, Created)
DT 01-PEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Her/33) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11187;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
```

```
RL Virology 169:273-282 (1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC -----
CC EMBL; M24702; AAA46652.1; -.
CC PIR; A36830; A36830.
CC InterPro; IPR000776; Fusion_gly.
CC Pfam; PF00523; fusion_gly.
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
CC Lipoprotein; Palmitate.
CC SIGNAL 1 25
CC CHAIN 26 553 FUSION GLYCOPROTEIN F0.
CC CHAIN 26 116 F2 PROTEIN.
CC CHAIN 117 553 F1 PROTEIN.
CC TRANSMEM 117 136 POTENTIAL.
CC DOMAIN 137 500 EXTRACELLULAR.
CC TRANSMEM 501 527 POTENTIAL.
CC DOMAIN 528 553 CYTOPLASMIC.
CC CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 447 447 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 471 471 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 523 523 S-palmitoyl cysteine (in host)
CC LIPID
CC SEQUENCE 553 AA; 59129 MW; F7F39B3F7BC031B0 CRC64;
CC -----
CC Query Match 94.2%; Score 2598; DB 1; Length 553;
CC Best Local Similarity 94.4%; Pred. No. 1.7e-154;
CC Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
CC -----
CC 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGKAVNIYTSQGS 60
CC 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAGIVVTGKAVNIYTSQGS 60
CC -----
CC 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQESVTTSGGKQRLIGA 120
CC 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTFLGDSIRRIQESVTTSGGKQRLIGA 120
CC -----
CC 121 IIGGAALGVATAQITAAASALIQANQANAILRLKERIAATNEAVHEVTDGLSQAIVAG 180
CC 121 IIGGAALGVATAQITAAASALIQANQANAILRLKERIAATNEAVHEVTDGLSQAIVAG 180
CC -----
CC 121 IIGSVALGVATAQITAAASALIQANQANAILRLKESIAATNEAVHEVTDGLSQAIVAG 180
CC 121 IIGSVALGVATAQITAAASALIQANQANAILRLKESIAATNEAVHEVTDGLSQAIVAG 180
CC -----
CC 181 KMQQFVNDQFNKTAQELDCIKITQQGVGLNLYLTTLTVFGPOITSPALQTQIALYN 240
CC 181 KMQQFVNDQFNKTAQELDCIKITQQGVGLNLYLTTLTVFGPOITSPALQTQIALYN 240
CC -----
CC 241 LAGNMDYLLTKLGVGNQNLSSLSGLITGNPLIYDSQTLQLGIQVTLPSVGNLNMRA 300
CC 241 LAGNMDYLLTKLGVGNQNLSSLSGLITGNPLIYDSQTLQLGIQVTLPSVGNLNMRA 300
CC -----
CC 301 TYLETLSVSTTKGFASALVPKVMKGVSVTEELDTSCYIEDTDLXCTRIVTTPMSPGIY 360
CC 301 TYLETLSVSTTKGFASALVPKVMKGVSVTEELDTSCYIEDTDLXCTRIVTTPMSPGIY 360
CC -----
CC 361 SCLSGNTSACWYKTEGALTTPYMLKGVSVIANCKMTTCRCADPPGIIISYNGEASLID 420
CC 361 SCLSGNTSACWYKTEGALTTPYMLKGVSVIANCKMTTCRCADPPGIIISYNGEASLID 420
CC -----
CC 421 RQSCNVLSLGDITLRLSGEFDATYQKNISILDQSVIVTGNLDISTELGNVNNISNALDK 480
CC 421 RQSCNVLSLGDITLRLSGEFDATYQKNISILDQSVIVTGNLDISTELGNVNNISNALDK 480
CC -----
Db 421 RHCNVLSLGDITLRLSGEFDATYQKNISILDQSVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEENSKLDKVNKLTSTLSALITVITVIVSLVCGILSLVACLYMYKQKQKQKQKQKQK 540
Db 481 LEENSKLDKVNKLTSTLSALITVITVIVSLVCGILSLVACLYMYKQKQKQKQKQKQK 540
Qy 541 NNTLDQMRATTQM 553
Db 541 NNTLDQMRATTKI 553
CC -----
CC RESULT 9
CC VGLF_NDVTG
CC ID_VGLF_NDVTG STANDARD; PRT; 553 AA.
CC AC P12571;
CC DT 01-OCT-1989 (Rel. 12, Created)
CC DT 10-OCT-1989 (Rel. 12, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
CC GN Fusion glycoprotein F1].
CC OS Newcastle disease virus (strain Texas G.b./48) (NDV).
CC OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
CC OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
CC OX NCBI_TaxID=11189;
CC RN [1]
CC RP MEDLINE=88265873; PubMed=3388773;
CC RX MEDLINE=89204898; PubMed=2705298;
CC RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
CC RA Nagai Y.;
CC RT "Newcastle disease virus evolution. II. Lack of gene recombination in
CC RL Virology 169:273-282 (1989).
CC CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M23407; AAA46642.1; -.
CC EMBL; M24698; AAA46649.1; -.
CC PIR; G46329; G46329.
CC InterPro; IPR000776; Fusion_gly.
CC Pfam; PF00523; fusion_gly.
CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
CC Lipoprotein; Palmitate.
CC SIGNAL 1 25
CC CHAIN 26 553 FUSION GLYCOPROTEIN F0.
CC CHAIN 26 116 F2 PROTEIN.
CC CHAIN 117 553 F1 PROTEIN.
CC TRANSMEM 117 136 POTENTIAL.
CC DOMAIN 137 500 EXTRACELLULAR.
CC TRANSMEM 501 527 POTENTIAL.
CC DOMAIN 528 553 CYTOPLASMIC.
CC CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host)
                                         (potential).
SQ SEQUENCE 553 AA; 59017 MW; 5F537269FE76F9E9 CRC64;

Query Match 94.1%; Score 2593; DB 1; Length 553;
Best Local Similarity 93.1%; Pred. No. 3.6e-154;
Matches 515; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGPRESTKNTPTVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPGLGDSIRRIQESVTTSGGKGQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPGLGDSIRRIQESVTTSGGKGQRLIGA 120

QY 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180
DB 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180

QY 121 IIGGVALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180
DB 121 IIGGVALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLTVFGPQITSPALTOITQALYN 240

QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCYTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCYTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420

QY 421 ROSCNVLSIDGTLRLSGFDATYQKNISIQDSQVIVTGNLIDISTELGVNNSISNALDK 480
DB 421 ROSCNVLSIDGTLRLSGFDATYQKNISIQDSQVIVTGNLIDISTELGVNNSISNALDK 480

QY 481 LEESKLDKNNVLTSTTSALITYLVISLVCGLSILVACILMYKKAQOKTLMLG 540
DB 481 LEESKLDKNNVLTSTTSALITYLVISLVCGLSILVACILMYKKAQOKTLMLG 540

QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

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RESULT 10
VGLF NDVI STANDARD; PRT; 553 AA.
AC P14623;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Italien/45) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11182;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87240797; PubMed=3592986;
RA Espion D., de Henau S., Letellier C., Wemmers C.-D., Brasseur R.,
RA Young J.F., Gross M., Rosenberg M., Meulemans G., Burny A.;
RT "Expression at the cell surface of native fusion protein of the
RT Newcastle disease virus (NDV) strain Italian from cloned cDNA.";

```

```

Arch. Virol. 95:79-95 (1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=89204898; PubMed=2705298;
RX Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RA "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282 (1989). directs fusion of viral and cellular
CC -1- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC
CC -----
CC EMBL; M17710; AAA46640.1; -.
CC FUSION GLYCOPROTEIN FO.
DR EMBL; M24703; AAA46653.1; ALT_SEQ.
DR PIR; B36830; B36830.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
FT SIGNAL 1 25
FT CHAIN 26 553
FT CHAIN 117 553
FT CHAIN 117 553
FT TRANSMEM 117 136
FT DOMAIN 137 500
FT TRANSMEM 501 527
FT DOMAIN 528 553
FT CARBOHYD 85 85
FT CARBOHYD 191 191
FT CARBOHYD 366 366
FT CARBOHYD 447 447
FT CARBOHYD 471 471
FT LIPID 523 523
FT CONFLICT 289 290
FT CONFLICT 339 339
FT CONFLICT 491 491
SQ SEQUENCE 553 AA; 59260 MW; 639B2F2AE19153E2 CRC64;

Query Match 93.9%; Score 2588; DB 1; Length 553;
Best Local Similarity 93.9%; Pred. No. 7.3e-154;
Matches 519; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGRSSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPGLGDSIRRIQESVTTSGGKGQRLIGA 120
DB 61 IIVKLLPNMPKDEKACAPLEAYNRTLTLLTPGLGDSIRRIQESVTTSGGKGQRLIGA 120

QY 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180
DB 121 IIGGAALGVATAAQITTAASALIQANNAANILRLKERTAAATNEAVEHVTGDSQLAVAG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLTVFGPQITSPALTOITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETLTVFGPQITSPALTOITQALYN 240

QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

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Db 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCMETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSNVSACMYSKTEGALTPPYMTLKGSVIANCWMTTCRCADPRGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTPPYMALKGVSVIANCWMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSOVITVGNLDISTELGNVANSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFDATYQKNISILDSQVITVGNLDISTELGNVANSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVLVISLVCGILSLVACVLMYKQKQAQKTLMLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITIVLVISLVFGVLSVLVACVLMYKQKQAQKTLMLWG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 11
VGLF NDVL
ID VGLF NDVL STANDARD; PRT; 553 AA.
AC P33614;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Las/46) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11184;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89204898; PubMed=2705298;
RA Toyoda T., Sakaguchi T., Hirota H., Gotoh B., Kuma K., Miyata T.,
RA Nagai Y.;
RT "Newcastle disease virus evolution. II. Lack of gene recombination in
RT generating virulent and avirulent strains.";
RL Virology 169:273-282(1989).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
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CC -----
CC EMBL; M24696; AAA46647.1; -.
DR PIR; E46329; E46329.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal;
KW Lipoprotein; Palmitate.
FT SIGNAL 1 25
FT CHAIN 26 553 FUSION GLYCOPROTEIN F0.
FT CHAIN 26 116 F2 PROTEIN.
FT CHAIN 117 553 F1 PROTEIN.
FT TRANSMEM 117 136 POTENTIAL.
FT DOMAIN 137 500 EXTRACELLULAR.
FT TRANSMEM 501 527 POTENTIAL.
FT
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FT DOMAIN 528 553 CYTOPLASMIC.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 523 523 S-palmitoyl cysteine (in host
SQ SEQUENCE 553 AA; 59047 MW; 04E11F38573B91DF CRC64;
Query Match 93.9%; Score 2588; DB 1; Length 553;
Best Local Similarity 92.6%; Pred. No. 7.3e-154;
Matches 512; Conservative 21; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVCPSTSLDQRPLAAAGIVVTGKAVNIYTSQTGS 60
Db 1 MGRSPSTKIPAPMLTIRVALVLSICFPANSIDGRPLAAAGIVVTGKAVNIYTSQTGS 60
Qy 61 IIVKLLNMPKDKKACAKAPLEAVNRTLTTLLTLPGLDSIRRIQSVTSSGGKQRLIGA 120
Db 61 IIVKLLNPLPKDKKACAKAPLDAYNRTLTTLLTLPGLDSIRRIQSVTSSGGKQRLIGA 120
Qy 121 IIGGAALGVATAAOITAAASALIQANQNAANLRLKERTAAATNEAVHEVTDGLSOIAVAVG 180
Db 121 IIGGVALGVATPAQITAAALIQAKNAANLRLKESIAATNEAVHEVTDGLSOIAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQGVGVELNLYLTTLTTFVFGPOITSPALTLQIALYN 240
Db 181 KMQQFVNDQFNKTAQELDWIKIAQGVGVELNLYLTTLTTFVFGPOITSPAFNKLTIQIALYN 240
Qy 241 LAGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNRA 300
Db 241 LAGNMDYLLTKLGVGNQSLISGLITGNPIYDSQTLGIQITSPSVGNLNNRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 SYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTPPYMTLKGSVIANCWMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEAALTTPPYMTIRKSVIANCWMTTCRCVNPFGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSOVITVGNLDISTELGNVANSISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIODSOVITVGNLDISTELGNVANSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVLVISLVCGILSLVACVLMYKQKQAQKTLMLWG 540
Db 481 LEESNRKLDKVNKLTSTSAITIVLVISLVFGVLSVLVACVLMYKQKQAQKTLMLWG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553
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RESULT 12
VGLF NDVM
ID VGLF NDVM STANDARD; PRT; 553 AA.
AC P10855;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Newcastle disease virus (strain Miyadera/51) (NDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11185;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=87207668; PubMed=3576973;
RA Toyoda T., Sakaguchi T., Imai K., Inocencio N.M., Gotoh B.,
```


QY 369 ACWYKTEGALTPYMTLKGSIANCKMTTCRCADPPGIISQNYGEAVSLIDROSCNVLS 428
Db 355 ACVSPAGSYMRFEALDGIIVANCRLTCLCKSPSPYIQPDHATVITDLTACQTL 414
QY 429 LOGITRLSGEDFATYQKNIQSDQSVITGNLDISTELGNVNSISNALDKLESNKL 488
Db 415 LDGLDFSVLSNITYAENLATSLSQTINTQPIDISTELSKVNASLQNAVYKESNHL 474
QY 489 DKVNYKLTSTALITYIVITVLSVCGILSLVLA 524
Db 475 QSVNNSKIGAITVAALVLSLSI---IISLFCWC 507

RESULT 15
VGLF P12H STANDARD; PRT; 551 AA.
AC P25467;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Human parainfluenza 2 virus (PIV-2).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11212;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91049467; PubMed=2173268;
RA Hu X., Compans R.W., Matsuoaka Y., Ray R.;
RT "Molecular cloning and sequence analysis of the fusion glycoprotein
RT gene of human parainfluenza virus type 2.";
RL Virology 179:915-920(1990).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M60182; AAA46843.1; -.
CC HSP; P04849; 1SVF.
CC InterPro; IPR000776; Fusion gly.
CC Pfam; PF00523; fusion_gly; 1.
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 551 FUSION GLYCOPROTEIN FO.
FT CHAIN 26 106 F2 PROTEIN.
FT CHAIN 107 551 F1 PROTEIN.
FT TRANSMEM 107 132 IMPORTANT ROLE IN MEMBRANE FUSION
FT ACTIVITY (POTENTIAL).
FT TRANSMEM 486 513 POTENTIAL.
FT DISULFID 68 189 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 551 AA; 59668 MW; 0003A2635A3AA0C8 CRC64;

Query Match 25.6%; Score 706; DB 1; Length 551;
Best Local Similarity 33.2%; Pred. No. 1e-36;
Matches 165; Conservative 105; Mismatches 217; Indels 10; Gaps 6;

QY 29 TSSLDGRPLAAGIVTGDKAVNIYTSSTQSGIIIVKLLPNMPKDEACAKAPLEAVNRTL 88
Db 21 SDATAGDQLLNGIVQSKIRSLMYTDDGASFIWVKLLPNLPSPNGTNIITSLDAYNVTL 80
QY 89 TTLTLPGLGDSIRRIQESVTTSGGGKQGRLLIGAIIGGAALGVATAAQITAAASALIIOANQNA 148
Db 81 FKLLTPLIENLSKI--STVTDTKTRKRFAGVWVGLAALGVATAAQITAAVAIVKANANA 138
QY 149 ANILRLKERIAATNEAVHEVTDGLSOLAVAVKMQOQFVNDQFNKTAQELDCIKITQOQGV 208
Db 139 AAINNLAASSIQSTNKAUSDVIDASRTIATAVQAIQDHINGAIVNGITSASCRADHALLGS 198
QY 209 ELNLYLTETTVFGPQITSPALTOLTIOALYNLAGNMDYLL-TKLGVGNOLSLIGSG 267
Db 199 IINLYLTETTVTFHNOITNPALTPLISQALRIILGSTLPVIESKINT-NLNTALLSSG 257
QY 268 LITGNPILYDSQTQLLGIQVTLPSVGNLNNRATYLETSLVSTTTKGPASAL--VPKVMK 325
Db 258 LLTGQIISISPMYMQMLIQINVPTF--IMQPGAKVIDLIAISANHKLOEVVVVQVNPRI 315
QY 326 VGSVIEELDTSYCIETDLDLYCTRIVTTPMSPGIYSCLSGNTSACWYKTEGALTTPYMT 385
Db 316 YANELQNYPANDCVVTPNSVFCRYNEGSPIPESQYQCLRGNLNSCTFTPIIGNFLKRF 375
QY 386 LKGSVIANCKMTTCRCADPPGIISQNYGEAVSLIDROSCNVLSLDGITRLSGEDATYQ 445
Db 376 ANGVLYANCKSLCCADPPHVVSQDDTQGISIIDIKCESEMMLDTFFSRTISTENATYV 435
QY 446 KNISQDSQVITVGNLDISTELGNVNSISNALDKLESNKLDKVNVKLTSTALITYI 505
Db 436 TDFSMINANIIVHLSPLDLSNQINSINKLSKAEDWIADSNFFANQARTAKTIYLSL 495
QY 506 VLTWISLVCGILSLVLA 522
Db 496 ILSVITLV--VWGLLIA 510

Search completed: April 18, 2004, 01:07:20
Job time : 42 secs


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QY 121 IIGGAALGVATAAOITAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGGVALGVATAAOITAAASALIQANONAAANILRLKESIAATNEAVHEVINGLSQAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDTITRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVANSISNALDK 480
DB 421 ROSCNVLSLDTITRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVANSISNALDK 480
QY 481 LEESNKLDKVNKLTSTSAITYIVLVISLVCGLSLVACYLMYKQKQKQKTLMLG 540
DB 481 LEESNKLDKVNKLTSTSAITYIVLVISLVCGLSLVACYLMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 2
Q83855 PRELIMINARY; PRT; 553 AA.
AC Q83855;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE F protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]_TaxID=11176;
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster mutant;
RX MEDLINE=90261333; PubMed=2188464;
RA Pritzer E., Kuroda K., Garten W., Nagai Y., Klenk H.P.;
RT "A host range mutant of Newcastle disease virus with an altered
RT cleavage site for proteolytic activation of the F protein.";
RL Virus Res. 15:237-242(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster mutant;
RA Garten W.D.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; 212110; CA478095.1; -.
DR PIR; S23621; S23621.
DR PIR; S38785; S38785.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex; IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR GO; GO:0019039; F:viral-cell fusion molecule activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion Gly.
DR InterPro; IPR000685; Rubisco large.
DR Pfam; PF00523; fusion gly; 1.
SQ SEQUENCE 553 AA; 58959 MW; D478E1A51A6EAD8 CRC64;

Query Match 96.4%; Score 2658; DB 12; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.8e-163;
Matches 524; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQBSVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQBSVTTSGGKQRLIGA 120
QY 121 IIGGAALGVATAAOITAAASALIQANONAAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGGVALGVATAAOITAAASALIQANONAAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTELTTVFPGQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDTITRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVANSISNALDK 480
DB 421 ROSCNVLSLDTITRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVANSISNALDK 480
QY 481 LEESNKLDKVNKLTSTSAITYIVLVISLVCGLSLVACYLMYKQKQKQKTLMLG 540
DB 481 LEESNKLDKVNKLTSTSAITYIVLVISLVCGLSLVACYLMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 3
Q776W0 PRELIMINARY; PRT; 553 AA.
AC Q776W0;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]_TaxID=11176;
RP SEQUENCE FROM N.A.
RC STRAIN=Luoyi;
RA Hu R., Bao S., Zhang S.;
RT "Molecular epidemiological investigation of different strains of
RT Newcastle disease virus.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY341061; AAQ16124.1; -.
SQ SEQUENCE 553 AA; 59016 MW; 20F113CEE2D9E194 CRC64;

Query Match 95.1%; Score 2623; DB 12; Length 553;
Best Local Similarity 94.8%; Pred. No. 3.3e-161;
Matches 524; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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```
QY 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
DB 1 MGSRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
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QY 61 IIVKLLPNPKDKEACAKAPLEAYNRLTLLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRLTLLTLLPLGDSIRRIQESVTTSGGKQGRFFGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGSVALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQQVGVVELNLYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMOQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db 241 LAGGNDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCVETDLDLYCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTIKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYOKNISTQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFDTYQKNISLDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LBEESKLDKVNKLTSTALITVIVLTIVLSVCGILSLVLACVLMYKQKAAQKTLILWL 540
Db 481 LBEESKLDKVNKLTSTALITVIVLTIVLSVCGILSLVLACVLMYKQKAAQKTLILWL 540
QY 541 NNTLDQWRATT 551
Db 541 NNTLDQWRATT 551

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RESULT 4

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Q8Q25 ID Q8Q25 PRELIMINARY; PRT; 551 AA.
AC Q8Q25;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-1/85;
RA Ni X., Wu Y., Liu X.;
RT "Molecular epizootiological study of chicken Newcastle disease (ND) in
RT east China.";
RL Zhongguo jiaqin 0:0-0(2002).
DR EMBL; AF458009; AML3424.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
FT NON_TER 551
SQ SEQUENCE 551 AA; 58730 MW; 93CE2D9E1947BFA CRC64;

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Query Match 95.1%; Score 2621; DB 12; Length 551;
 Best Local Similarity 95.1%; Pred. No. 4.4e-161;
 Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTDKAVNIYTSOTGS 60
Db 1 MGPKSSTNVPAFLMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRLTLLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

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Db 61 IIVKLLPNPKDKEACAKAPLEAYNRLTLLTLLPLGDSIRRIQESVTTSGGKQGRFFGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGSVALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQQVGVVELNLYLTTELTTVFGPQITSPALTIQALYN 240
Db 181 KMOQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTTELTTVFGPQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db 241 LAGGNDYLLTKLGVGNQNLSSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCVETDLDLYCTRIIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTIKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYOKNISTQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFDTYQKNISLDSQVIVTGNLDISTELGNVNNISNALDK 480
QY 481 LBEESKLDKVNKLTSTALITVIVLTIVLSVCGILSLVLACVLMYKQKAAQKTLILWL 540
Db 481 LBEESKLDKVNKLTSTALITVIVLTIVLSVCGILSLVLACVLMYKQKAAQKTLILWL 540
QY 541 NNTLDQWRATT 551
Db 541 NNTLDQWRATT 551

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RESULT 5

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Q8V1Q7 ID Q8V1Q7 PRELIMINARY; PRT; 551 AA.
AC Q8V1Q7;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JS/1/97/Go;
RA Wan H., Wu Y., Liu X., Zhang R.;
RT "Sequence analysis of the fusion (F) protein genes of four Newcastle
RT disease virus strains causing clinical disease in geese.";
RL Wei Sheng Wu Heueh Pao 0:0-0(2002).
DR EMBL; AF456435; AAL57897.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion gly; I.
FT NON_TER 551
SQ SEQUENCE 551 AA; 58730 MW; 93CEE2D9E1947BFA CRC64;

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Query Match 95.1%; Score 2621; DB 12; Length 551;
 Best Local Similarity 95.1%; Pred. No. 4.4e-161;
 Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MGRSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTDKAVNIYTSOTGS 60
Db 1 MGPKSSTNVPAFLMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTDKAVNIYTSOTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRLTLLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120

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Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGRRQRFICA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGSVALGVATAAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTVFGPQITSPALTIQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKVSIVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKVSIVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFDVYQKNISILDSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEENSCKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLWLG 540
Db 481 LEENSCKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLWLG 540
QY 541 NNTLDQMRATT 551
Db 541 NNTLDQMRATT 551
```

RESULT 6

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Q80KD0 PRELIMINARY; PRT; 551 AA.
ID Q80T13
AC Q80T13;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JS-1/97;
RA Ni X., Wu Y., Liu X.;
RT "Molecular epizootiological study of chicken Newcastle disease (ND) in
east China.";
RL Zhongguo jiaqin 0:0-0(2002).
DR EMBL; AF458022; AAM13436.1; -
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
FT NON TER 551
SQ SEQUENCE 551 AA; 58730 MW; 93CEE2D9E1947BFA CRC64;
```

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Query Match 95.1%; Score 2621; DB 12; Length 551;
Best Local Similarity 95.1%; Pred. No. 4.4e-161;
Matches 524; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
Db 1 MGPKSSTNVAPAPMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGKQGRLIGA 120
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Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESATTSGGRRQRFICA 120
QY 121 IIGGAALGVATAAQITTAASALIQAQNAANILRLKERIAATNEAVHEVTDGLSQLAVAG 180
Db 121 IIGSVALGVATAAQITTAASALIQAQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNYLTTELTVFGPQITSPALTIQALYN 240
QY 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNMNDYLLTKLGVGNQSLIGSLITGNPIYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKVSIVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVMKVSIVBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIODSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFDVYQKNISILDSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEENSCKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLWLG 540
Db 481 LEENSCKLDKVNKLTSTLSALITYIVLTVISLVCGLSLVACVIMYKQKQOQKTLWLG 540
QY 541 NNTLDQMRATT 551
Db 541 NNTLDQMRATT 551
```

RESULT 7

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Q80KD0 PRELIMINARY; PRT; 553 AA.
ID Q80KD0
AC Q80KD0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fusion protein.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB92;
RA Pan Z.S., Chen Y.D., Shao H.B., Yang J., Xiong Z.L., Wen G.Y.,
RA Zhang C.Y.;
RT "Complete sequence for HB92 strain of Newcastle disease virus.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB92;
RA Shao H.B., Yang J., Xiong Z.L.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225110; AAO46783.1; -
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58866 MW; E336AEF87E9D655E CRC64;
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Query Match 95.1%; Score 2621; DB 12; Length 553;
Best Local Similarity 93.7%; Pred. No. 4.4e-161;
Matches 518; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
Db 1 MGRSSSTNVAPAPMLTVRIALALSCVRLTNSLDGRPLAAAGIVVTGDKAVNIYTSSTQGS 60
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QY 61 IIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDKCAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGALGVATAAQITAAASALIQAQNAANIILRLKERIAATNEAVEHVDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAALIOAKQNAANIILRLKESIAATNEAVEHVDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTTFVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTTLTTFVFGPQITSPALNKLTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTRKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGFEDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGFEDVYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNKLKDVNKLSTTSALITYIVLTISLVCGILSLVLAACYLMYKQKQKTLMLWG 540
DB 481 LEESNKLKDVNKLSTTSALITYIVLTISLVFGILSLILACYLMYKQKQKTLMLWG 540
QY 541 NNTLQDMRATTKM 553
DB 541 NNTLQDMRATTKM 553

RESULT 8
Q9NMH7
ID Q9NMH7 PRELIMINARY; PRT; 553 AA.
AC Q9NMH7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20047980; PubMed=10580061;
RA Roemer-Oberdorfer A., Mundt E., Mebatsion T., Buchholz U.J.,
RA Mettenleiter T.C.;
RT "Generation of recombinant lentogenic Newcastle Disease Virus from
RT cDNA.";
RL J. Gen. Virol. 80:2987-2995(1999).
RN [2]
SEQUENCE FROM N.A.
RP Roemer-Oberdorfer A.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18898; CAB51325.1; -.
DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion gly.
DR Pfam; PF00523; fusion_gly; I.
SQ SEQUENCE 553 AA; 58868 MW; 1D2D10C09DC6E36B CRC64;

Query Match 95.0%; Score 2619; DB 12; Length 553;
Best Local Similarity 93.7%; Pred. No. 6e-161;
Matches 518; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
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QY 1 MGSRSSTRIPVPMITVRVALALSVCPTSSSIDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
DB 1 MGSRPSSTKPNAPMMLTIRVALVLSCTPCPANSIDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
QY 61 IIVKLLPNMPKDKCAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDKCAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGALGVATAAQITAAASALIQAQNAANIILRLKERIAATNEAVEHVDGLSOLAVAG 180
DB 121 IIGGVALGVATAAQITAAALIOAKQNAANIILRLKESIAATNEAVEHVDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTTFVFGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTTLTTFVFGPQITSPALNKLTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNDYLLTKLGVGNOLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTRKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGFEDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITRLSGFEDVYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNKLKDVNKLSTTSALITYIVLTISLVCGILSLVLAACYLMYKQKQKTLMLWG 540
DB 481 LEESNKLKDVNKLSTTSALITYIVLTISLVFGILSLILACYLMYKQKQKTLMLWG 540
QY 541 NNTLQDMRATTKM 553
DB 541 NNTLQDMRATTKM 553

RESULT 9
O90339
ID O90339 PRELIMINARY; PRT; 553 AA.
AC O90339;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein F.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=LaSota;
RX MEDLINE=99131394; PubMed=9934695;
RA de Leeuw O., Peeters B.;
RT "Complete nucleotide sequence of Newcastle disease virus: evidence for
RT the existence of a new genus within the subfamily Paramyxovirinae.";
RL J. Gen. Virol. 80:131-136(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=LaSota;
RA de Leeuw O.S., Peeters B.P.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=27/2000;
RA Zhou J.Y., Ye J.X., Chen Q.X., Chen J.G., Cheng L.Q., Wang J.Y.;
RT "Newcastle disease virus Strain ZJ/2000.";
```

Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF077761; AAC28374.1; -
DR EMBL: AF534997; AAN01226.1; -
DR GO: 0019039; F: viral-cell fusion molecule activity; IEA.
DR GO: 0006948; F: viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58896 MW; 4D29AEF87E4255B0 CRC64;

Query Match 94.9%; Score 2616; DB 12; Length 553;
Best Local Similarity 93.5%; Pred. No. 9.3e-161;
Matches 517; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVPTSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
QY 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAALIOAANAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGVALGVATAAQITAAALIOAANAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNLMNLYLTTLTVFGPOITSPALNTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNLMNLYLTTLTVFGPOITSPALNTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSCIEFDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNRKLDKVNKLTSTALITVITVLSLVCGLSLVLAACVLMYKQAKQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITVITVLSLVCGLSLVLAACVLMYKQAKQKTLWLIG 540
QY 541 NNTLDQMRATTM 553
DB 541 NNTLDQMRATTM 553

RESULT 10
Q91AH8 PRELIMINARY; PRT; 553 AA.
AC Q91AH8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B1;
RX MEDLINE=21548317; PubMed=11689669;
RA Nakaya T., Cros J., Park M.S., Nakaya Y., Zheng H., Sagrera A.,
Villar E., Garcia-Sastre A., Palese P.

"Recombinant newcastle disease virus as a vaccine vector.";
J. Virol. 75:11868-11873 (2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=B1;
RA Nakaya T., Garcia-Sastre A., Palese P.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF375823; AAK55550.1; -
DR GO: 0019039; F: viral-cell fusion molecule activity; IEA.
DR GO: 0006948; F: viral-induced cell-cell fusion; IEA.
DR InterPro: IPR000776; Fusion_gly.
DR Pfam: PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58910 MW; F09767CFDCE4493 CRC64;

Query Match 94.8%; Score 2615; DB 12; Length 553;
Best Local Similarity 93.3%; Pred. No. 1.1e-160;
Matches 516; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVPTSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
DB 1 MGRSPSTKNPAPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
QY 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAALIOAANAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGVALGVATAAQITAAALIOAANAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNLMNLYLTTLTVFGPOITSPALNTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNLMNLYLTTLTVFGPOITSPALNTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGNMDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCIEFDLDLYCTRIVTFPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSCIEFDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNRKLDKVNKLTSTALITVITVLSLVCGLSLVLAACVLMYKQAKQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTALITVITVLSLVCGLSLVLAACVLMYKQAKQKTLWLIG 540
QY 541 NNTLDQMRATTM 553
DB 541 NNTLDQMRATTM 553

RESULT 11
Q8QTL2 PRELIMINARY; PRT; 551 AA.
ID Q8QTL2
AC Q8QTL2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fusion protein (fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.

```
RC STRAIN=Zbj-1/85;
RA Ni X., Wu Y., Liu X.;
RT "Molecular epizootiological study of chicken Newcastle disease (ND) in
RL east China.";
RL Zongguo jiaqing 0:0-0(2002).
DR EMBL; AF458023; AM13437.1;
DR GO; GO:0019039; F: viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P: viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
FT NON TER 551
SQ SEQUENCE 551 AA; 58672 MW; 870A15D9E1947FA3 CRC64;

Query Match 94.7%; Score 2612; DB 12; Length 551;
Best Local Similarity 94.7%; Pred. No. 1.7e-160;
Matches 522; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNYTSSOTGS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 MGPKSTNVAPLMLTARIALALSCVLTSLDGRPLAAAGIVVTGDKAVNYTSSOTGS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQRLIGA 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESATTSGRRRFFIGA 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 IIGGALGVATAAQITAAASALIQANONAAANILRKERIAATNEAVHEVTDGLSOLAVAG 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 IIGSVALGVATAAQITAAASALIQANONAAANILRKESIAATNEAVHEVTDGLSOLAVAG 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTVFGPQITSPALTIQALYN 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNLYLTTLTVFGPQITSPALTIQALYN 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 LAGNMDYLLTKLGVGNQNLSSLIIGSLITGNPLDYDSOTQLLGIQVTLPSVGNLNMRA 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 LAGNMDYLLTKLGVGNQNLSSLIIGSLITGNPLDYDSOTQLLGIQVTLPSVGNLNMRA 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 RQCNVLSLGDITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 RHCNVLSLGDITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 LEESNKLKDVNKLSTSLALITYIVLTIVLSVCGILSLVLCYLYMYKQAKOQKLLWL 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 LEESNKLKDVNKLSTSLALITYIVLTIVLSVCGILSLVLCYLYMYKQAKOQKLLWL 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 NNTLDQMRATT 551
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 NNTLDQMRATT 551
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q9WLE2 PRELIMINARY; PRT; 553 AA.
ID Q9WLE2
AC Q9WLE2;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=DB5;
RA Cao D.J., Yuan C.X., Guo X., Min P., Kong X.G., Lu J.L.;
RT "Genetic Variance Analysis of F Gene of NDV From China.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079323; AAC62244.1;
DR GO; GO:0019039; P: viral-cell fusion molecule activity; IEA.
DR GO; GO:0006948; P: viral-induced cell-cell fusion; IEA.
DR InterPro; IPR000776; Fusion_gly.
DR Pfam; PF00523; fusion_gly; 1.
SQ SEQUENCE 553 AA; 58912 MW; 513469F7DDB805B4 CRC64;

Query Match 94.7%; Score 2611; DB 12; Length 553;
Best Local Similarity 93.3%; Pred. No. 2e-160;
Matches 516; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAAGIVVTGDKAVNYTSSOTGS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 MGSRPSTKNPAPWMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNYTSSOTGS 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQRLIGA 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQRLIGA 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 IIGGALGVATAAQITAAASALIQANONAAANILRKERIAATNEAVHEVTDGLSOLAVAG 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 IIGSVALGVATAAQITAAASALIQANONAAANILRKESIAATNEAVHEVTDGLSOLAVAG 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTVFGPQITSPALTIQALYN 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTTLTVFGPQITSPALTIQALYN 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 LAGNMDYLLTKLGVGNQNLSSLIIGSLITGNPLDYDSOTQLLGIQVTLPSVGNLNMRA 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 241 LAGNMDYLLTKLGVGNQNLSSLIIGSLITGNPLDYDSOTQLLGIQVTLPSVGNLNMRA 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIISQNYGEAVSLID 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 RQCNVLSLGDITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 421 KQCNVLSLGDITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 LEESNKLKDVNKLSTSLALITYIVLTIVLSVCGILSLVLCYLYMYKQAKOQKLLWL 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 481 LEESNKLKDVNKLSTSLALITYIVLTIVLSVCGILSLVLCYLYMYKQAKOQKLLWL 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 NNTLDQMRATT 553
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 541 NNTLDQMRATT 553
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q9WLE1 PRELIMINARY; PRT; 553 AA.
ID Q9WLE1
AC Q9WLE1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Fusion protein.
GN F.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ENDV1;
RA Cao D.J., Yuan C.X., Guo X., Min P., Kong X.G., Lu J.L.;
```

RT "Genetic Variance Analysis of F Gene of NDV From China.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079324; AAC62245.1; -;
 DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.
 DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; P:Viral-induced cell-cell fusion; IEA.
 DR Pfam; PF00523; fusion_gly; 1.
 SQ SEQUENCE 553 AA; 58969 MW; 6C181D049F971302 CRC64;

Query Match 94.5%; Score 2606; DB 12; Length 553;
 Best Local Similarity 93.1%; Pred. No. 4.1e-160;
 Matches 515; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
 Db 1 MGRSPSTKNPVPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
 Qy 61 IIVKLLPNMPDKKACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
 Db 61 IIVKLLPNLPDKKACAKAPLDAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
 Qy 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQSLAVAG 180
 Db 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQSLAVAG 180
 Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Qy 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Qy 421 ROSCNVLSDGITRLSGEFDATYQKNISIQDSQVITVGNLIDISTELGNVNNISNALDK 480
 Db 421 ROSCNVLSDGITRLSGEFDATYQKNISIQDSQVITVGNLIDISTELGNVNNISNALDK 480
 Qy 481 LEESNRKLDKVNKLTSTALITYVLTIVSLVCGILSLVACLYMYKQKQAKTLLWLG 540
 Db 481 LEESNRKLDKVNKLTSTALITYVLTIVSLVCGILSLVACLYMYKQKQAKTLLWLG 540
 Qy 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKM 553

RESULT 14
 Q9WD11 PRELIMINARY; PRT; 553 AA.
 ID Q9WD11
 AC Q9WD11
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fusion protein.
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 RN NCBI_TaxID=11176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sagrera A., Villar E.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF099661; AAD28333.1; -;
 DR GO; GO:0019039; F:Viral-cell fusion molecule activity; IEA.

DR GO; GO:0006948; P:Viral-induced cell-cell fusion; IEA.
 DR InterPro; IPR000776; Fusion gly.
 DR Pfam; PF00523; fusion_gly; 1.
 SQ SEQUENCE 553 AA; 58890 MW; 4DF02A800E4531A4 CRC64;

Query Match 94.5%; Score 2605; DB 12; Length 553;
 Best Local Similarity 93.1%; Pred. No. 4.8e-160;
 Matches 515; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
 Db 1 MGRSPSTKNPVPMMLTIRVALVLSICIPANSIDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
 Qy 61 IIVKLLPNMPDKKACAKAPLEAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
 Db 61 IIVKLLPNLPDKKACAKAPLDAYNRTLTLLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
 Qy 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQSLAVAG 180
 Db 121 IIGGALGVATAAQAITAASALIQANNAANILRLKERIAATNEAVEHVTGSLQSLAVAG 180
 Qy 181 KMQOFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Db 181 KMQOFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPQITSPALTKLTIQALYN 240
 Qy 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGNMDYLLTKLGVGNQSSLLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
 Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Db 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
 Qy 421 ROSCNVLSDGITRLSGEFDATYQKNISIQDSQVITVGNLIDISTELGNVNNISNALDK 480
 Db 421 ROSCNVLSDGITRLSGEFDATYQKNISIQDSQVITVGNLIDISTELGNVNNISNALDK 480
 Qy 481 LEESNRKLDKVNKLTSTALITYVLTIVSLVCGILSLVACLYMYKQKQAKTLLWLG 540
 Db 481 LEESNRKLDKVNKLTSTALITYVLTIVSLVCGILSLVACLYMYKQKQAKTLLWLG 540
 Qy 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKM 553

RESULT 15
 Q91HX4 PRELIMINARY; PRT; 553 AA.
 ID Q91HX4
 AC Q91HX4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fusion protein.
 OS Newcastle disease virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 RN NCBI_TaxID=11176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NDV-JL-1/97;
 RA Ningyi J.;
 RT "Variabilities Analysis of HN Protein Gene among the NDV Strain
 RT Changli and Strains Offshore."
 RL Chin. J. Vet. Sci. 20:328-331(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NDV-JL-1/97;
 RA Ningyi J., Xinglong W., Zhuang D.;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757

Sequence: 1 MGSRSSTRIPVPLMLTVRVA.....KTLMLGNNTLDQMRATTKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion protei
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 G46329	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 E46329	cell fusion glycop
17	2585	93.8	553	1 I46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23622	gene F protein - N
21	2554	92.6	553	2 S23620	F protein - Newcas
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZMM	cell fusion glycop
26	712.5	25.8	538	2 S52472	cell fusion protei
27	704	25.5	538	1 VGNZMS	cell fusion glycop
28	704	25.5	551	1 VGNZP2	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

ALIGNMENTS

RESULT 1

VGNZU1

cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/67)

N;Contains: fusion glycoprotein F1; fusion glycoprotein F2

C;Species: Newcastle disease virus

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000

C;Accession: A29823; C46329

R;Miller, N.S.; Chambers, P.; Emerson, P.T.

J. Gen. Virol. 69, 613-620, 1988

A;Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprotein

ns.

A;Reference number: A92799; MUID:88171450; PMID:3351479

A;Accession: A29823

A;Molecule type: mRNA

A;Residues: 1-553 <ML>

A;Cross-references: GB:D00243; NID:g222174; PIDN:BAA00173.1; PID:g222175

A;Experimental source: strain Ulster

R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virolgy 169, 273-282, 1989

A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A;Reference number: A46329; MUID:89204898; PMID:2705298

A;Accession: C46329

A;Molecule type: genomic RNA

A;Residues: 1-553 <TOY>

A;Cross-references: GB:M24694; NID:g293923; PIDN:AAA46645.1; PID:g293924

A;Experimental source: strain ULS/67

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F;118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>

F;495-528/Domain: transmembrane #status predicted <TMN>

F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;

Best Local Similarity 99.1%; Pred. No. 1.4e-162;

Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALALSCVPTSSLDGRLAAGIVVTDKAVNIYTSQTGS 60

Db 1 MGSRSSTRIPVPLMLTVRVALALSCVPTSSLDGRLAAGIVVTDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAPLEAYNRTLTLLTPLDGDSIRRIQESVTTSGGKQRLIGA 120

Db 61 IIVKLLPNPKDKEACAPLEAYNRTLTLLTPLDGDSIRRIQESVTTSGGKQRLIGA 120

QY 121 IIGGAALGVATAAQITAAASALITCAONAAITLRLKERTAAATNEAVHEVTDGLSOLAVG 180

Db 121 IIGGAALGVATAAQITAAASALITCAONAAITLRLKERTAAATNEAVHEVTDGLSOLAVG 180

Qy	181	KMOQFVNDQFNKTAQELDCIKITQOQGVVELNLYLTTELTVFGPQITSPALQTQLTQALYN	240
Db	181	KMOQFVNDQFNKTAQELDCIKITQOQGVVELNLYLTTELTVFGPQITSPALQTQLTQALYN	240
Qy	241	LAGNMDYLLTKLGVGNQLSSLIGSGLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA	300
Db	241	LAGNMDYLLTKLGVGNQLSSLIGSGLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKWTTCCRDAPPGIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKWTTCCRDAPPGIISQNYGEAVSLID	420
Qy	421	ROSCNVLSLDGTTLLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISINALDK	480
Db	421	ROSCNVLSLDGTTLLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISINALDK	480
Qy	481	LEESNKLDKVNVKLTSTTSALITYIVLTIVISLVCGILSLVLACYLWYKQAKQKTLMLG	540
Db	481	LEESNKLDKVNVKLTSTTSALITYIVLTIVISLVCGILSLVLACYLWYKQAKQKTLMLG	540
Qy	541	NNTLDDMRATTQK	553
Db	541	NNTLDDMRATTQK	553

RESULT 2

A:Accession: A46329
C: cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
N: Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A46329
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204896; PMID:2705298
A:Accession: A46329
A:Molecule type: genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24692; NID:g293919; PIDN:AAA46643.1; PID:g293920
C:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:118-528/Domain: transmembrane #status predicted <TMN>
F:85-191.366.447.471/Binding site: carboxylate (Asn) (covalent) #status predicted

[illegible]

Qy	241	LAGNMDYLLTKLGVGNNOSSLIGSGLLITGNPILYDSOTOLLGHQVTLTPSVGNLNNMRA	300
Db	241	LAGNMDYLLTKLGVGNNOSSLIGSGLLITGNPILYDSOTOLLGHQVTLTPSVGNLNNMRA	300
Qy	301	TYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Db	301	TYLETLSVSTTKGFASALVPKVMKGVSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANKMWTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANKMWTTCRCADPPGIIISQNYGEAVSLID	420
Qy	421	RQSCNVILSDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Db	421	RQSCNVILSDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNSISNALDK	480
Qy	481	LEESNKLDKVNVLTSTSAITYVLTVISIVCGILSLVLACYLIMYKQAKQKTLMLG	540
Db	481	LEESNKLDKVNVLTSTSAITYVLTVISIVCGILSLVLACYLIMYKQAKQKTLMLG	540
Qy	541	NTTLDQMRATTM	553
Db	541	NTTLDQMRATTM	553

RESULT 3

gene F protein - Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
C;Accession: S23621
R;Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
Virus Res. 13, 237-242, 1990
A;Title: A host range mutant of Newcastle disease virus with an altered cleavage site
A;Reference number: S23620; MUID:90261333; PMID:2188464
A;Accession: S23621
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-553 <PRL>
A;Cross-references: EMBL:121110
C;Superfamily: parainfluenza virus cell fusion protein

Query Match	97.6%;	Score 2691;	DB 2;	Length 553;
Best Local Similarity	98.2%;	Pred. No. 1.7e-160;		
Matches 543;	Conservative 1;	Mismatches 9;	Indels 0;	Gaps 0;
Qy	1	MGSRSTRIPVPLMLTVRVVALALSCVCPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGTS	60	
Db	1	MGSRSTRIPVPLMLTVRVVALALSCVRPTSSLDGRPLAAAGIVVTGDKAVNIYTSSTGTS	60	
Qy	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKGRLIGA	120	
Db	61	IIVLLKNMPKDEACAKAPLEAYNRTLTLTLLPLGDSIRRIQESVTTSGGKGRLIGA	120	
Qy	121	IIGGAALGVATAAQITAAALIQANQAAANILRLKERIAATNEAVHEVTDGLSOLAVAG	180	
Db	121	IIGGAALGVATAAQITAAALIQANQAAANILRLKESIAATNEAVHEVTDGLSOLAVAG	180	
Qy	181	KMQGFVNDQFNKTAQELDCIKITQOVGVELNLYLTETLTVFGPOITSPALTQTIAQYN	240	
Db	181	KMQGFVNDQFNKTAQELDCIKITQOVGVELNLYLTETLTVFGPOITSPALNQLTIAQYN	240	
Qy	241	LAGNMMDYLTKLGVGNQNLSSLIGSLITGNPTLYDSQTLQIGIQVTLPSVGNLNNMRA	300	
Db	241	LAGNMMDYLTKLGVGNQNLSSLIGSLITGNPTLYDSQTLQIGIQVTLPSVGNLNNMRA	300	
Qy	301	TYLETLSVSTTKGFASALPVKVMKGVSVIEELDTSYCIETDLLYCTRIVTFPMSPGIV	360	
Db	301	TYLETLSVSTTKGFASALPVKVVTVQVSGVIGELDTSYCIETDLLYCTRIVTFPMSPGIV	360	
Qy	361	SLCSGNTSACMYSTKEGALTTPPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID	420	

Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 4
B46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain Que/66)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: B46329
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: B46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24693; NID:G293921; PIDN:AAA4644.1; PID:G293922
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: Glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F:495-528/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 97.4%; Score 2684; DB 1; Length 553;
Best Local Similarity 97.3%; Pred. No. 4.5e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGSRSSTRIPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGVALGVATAAQITAAAGIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGGVALGVATAAQITAAAGIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Qy 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Qy 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Qy 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480

Db 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 5
S38785
gene F protein - Newcastle disease virus
C;Species: Newcastle disease virus
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S38785
R;Garten, W.D.
submitted to the EMBL Data Library, May 1992
A;Reference number: S22083
A;Accession: S38785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-553 <GAR>
A;Cross-references: EMBL:Z12110; NID:G60658; PIDN:CAA78095.1; PID:G60659
C;Superfamily: parainfluenza virus cell fusion protein

Query Match 96.4%; Score 2658; DB 2; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.9e-158;
Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGSRSSTRIPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGVALGVATAAQITAAAGIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGGVALGVATAAQITAAAGIQAQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLTVFGPQITSPALTOITQALYN 240
Qy 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQSLISGLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLCTRIYVTFPMSPGIY 360
Qy 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACWYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Db 421 ROSCNVSLDGIITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSAITIVITVLSVCGILSLVACVLMYKQAKOQKTLMLG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 6

H46329
cell fusion glycoprotein precursor - Newcastle disease virus
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: S07422; H46329
R:McGinnes, L.W.; Morrison, T.G.
Virus Res. 5, 343-356, 1986
A:Title: Nucleotide sequence of the gene encoding the Newcastle disease virus protein
A:Reference number: S07422; MUID:87044526; PMID:3776349
A:Accession: S07422
A:Molecule type: mRNA
A:Residues: 1-553 <MCG>
A:Cross-references: EMBL:M21881
A:Experimental source: strain Australia-Victoria
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: H46329
A:Molecule type: Genomic RNA
A:Residues: 1-65, 'H', 67-553 <TOY>
A:Cross-references: GB:M24700; NID:G293933; PIDN:AAA46650.1; PID:G293934
A:Experimental source: strain AUS/32
C:Genetics:

A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:25-116/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:112-116/Region: cleavage processing #status predicted
F:117-553/Product: cell fusion glycoprotein F1 #status predicted <PM>
F:499-526/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.2%; Score 2625; DB 1; Length 553;
Best Local Similarity 95.5%; Pred. No. 2.2e-156;
Matches 528; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGRSSSTPIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
DB 1 MGRSSSTPIPVPLMLTVRVALALSCVHLASSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEACAKAPLEAYNRTLLTLLPLGDSIRRIQESVTTSGGRRQRFIGA 120
QY 121 IIGNALGVATAAQTAAALIOANQNAANILRLKERTAAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQTAAALIOANQNAANILRLKESITATIEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTELTTVFQPIITSPTALQTITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTELTTVFQPIITSPTALQTITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCYTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCYTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLNGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGTLRLSGEFDTYQKNISIQDSQVITVGNLDISTELGNVNNSISNALDK 480
DB 421 RHSCNVLSLDGTLRLSGEFDTYQKNISILDSQVITVGNLDISTELGNVNNSISNALDK 480

QY 481 LEESNSKLDKVNKLTSTSTALITYIVLTVISVCGILSLVACLYMYKQAKOQKTLWLIG 540
DB 481 LEESNSKLDKVNKLTSTSTALITYIVLTVISVCGILSLVACLYMYKQAKOQKTLWLIG 540
QY 541 NNTLDQMRATTKM 553
DB 541 NNTLDQMRATTKM 553

RESULT 7

D46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain B1/47)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: D46329
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: D46329
A:Molecule type: Genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24695; NID:G293925; PIDN:AAA46646.1; PID:G293926
C:Genetics:

A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.1%; Score 2622; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 3.4e-156;
Matches 517; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGRSSSTPIPVPLMLTVRVALALSCVPTSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
DB 1 MGRSPSTKIPAPMMLTRIVLVLSCIPANSIDGRPLAAAGIVTGDKAVNIYSSQTGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLLTLLPLGDSIRRIQESVTTSGGKQRLIGA 120
DB 61 IIVKLLPNMPKDEACAKAPLDAYNRTLLTLLPLGDSIRRIQESVTTSGGRRQRLIGA 120
QY 121 IIGNALGVATAAQTAAALIOANQNAANILRLKERTAAATNEAVHEVTDGLSOLAVAG 180
DB 121 IIGSVALGVATAAQTAAALIOANQNAANILRLKESITATIEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTELTTVFQPIITSPTALQTITQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQGVVELNLYLTELTTVFQPIITSPTALQTITQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
DB 241 LAGGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCYTRIVTFPMSPGIY 360
DB 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEBELDTSYCIETDLDYCYTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCVNPFGIIISQNYGEAVSLID 420
QY 421 ROSCNVLSLDGTLRLSGEFDTYQKNISIQDSQVITVGNLDISTELGNVNNSISNALDK 480
DB 421 KQSCNVLSLDGTLRLSGEFDTYQKNISIQDSQVITVGNLDISTELGNVNNSISNALNK 480
QY 481 LEESNSKLDKVNKLTSTSTALITYIVLTVISVCGILSLVACLYMYKQAKOQKTLWLIG 540
DB 481 LEESNRKLDKVNKLTSTSTALITYIVLTVISVCGILSLVACLYMYKQAKOQKTLWLIG 540

Qy	541	NNTL	QMR	ATT	KM	553
Db	541	NNTL	QMR	ATT	KM	553

RESULT 8

VGZNZTE

cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas)
M:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A34663
J:Taylor, J.; Edbauer, C.; Rey-Senelonge, A.; Bouquet, J.F.; Norton, E.; Goebel, S.; Des
R. Virol. 64, 1441-1450, 1990
A:Title: Newcastle disease virus fusion protein expressed in a fowlpox virus recombinant
A:Reference number: A34663; MUID:90204652; PMID:2157037
A:Accession: A34663
A:Molecule type: genomic RNA
A:Residues: 1-553 <TAY>
A:Cross-references: EMBL:M33855; NID:g332369; PIDN:AAA46675.1; PID:g332370
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-116/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F:112-116/Region: cleavage processing #status predicted
F:117-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F:117-133/Domain: transmembrane #status predicted <TM1>
F:504-521/Domain: transmembrane #status predicted <TM2>
F:85,131,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      94.5%;   Score 2606;   DB 1;   Length 553;
Best Local Similarity 94.8%;   Pred. No. 3.4e-155;
Matches 524;   Conservative 9;   Mismatches 20;   Indels 0;   Gaps 0;

QY      1  MGRSSSTRIPVPLMLTVRVALALSCVCPSTSLDGRPLAAGIVVTGDKANNIYTSSTGTS 60
      ||||| : |||||
Db      1  MGRSSSTRIPVPLMLIIRTALTLSCLRLTSLDGRPLAAGIVVTGDKANNIYTSSTGTS 60

QY      61  IIVKLLPNMPKDEACAKAPLEAYNRITLTLLTPLGDSIRRIQSVVTSGGKGGRIG 120
      ||||| : |||||
Db      61  IIVKLLPNMPKDEVCAPLEAYNRITLTLLTPLGDSIRRIQSVVTSGGRRRPTGA 120

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QY	121	IIGGALGVATAAQITTAASALITQANQONAA	180	VTGLSOLAVAVG	180
Db	121	IIGGALGVATAAQITTAASALITQANQONAA	180	VTGLSOLAVAVG	180
QY	181	KMQQFVDFNFKTAQELDCIKITQGVGVELN	240	YITELTTFVFGPQITSPALTTQITQAALYN	240
Db	181	KMQQFVDFNFKTAQELDCIKITQGVGVELN	240	YITELTTFVFGPQITSPALTTQITQAALYN	240

[illegible]

	Qy	301	TYLETLVSSTTKGFASALVPKVMKVGVSEELDTSCIETDLDLYCTRIVTFPMSPGIY	360
			:	
	Dd	301	TYLETLVSSTTKGFASALVPKVTQTQGVSEELDTSCIGTDLDLYCTRIVTFPMSPGIY	360
			:	

[illegible]

421	RHSCNVLSDGTTLSGFEFATYQKNISILDSQVITVGTNLDISTELGNVNSISNALNK	480
Db		
Qy	LEESNKLDDKNNVKLTSTTSALITVLTIVSLVCGILSLVACLVMYKKQAQOKTLLWLG	540

Db 481 LEENS KLDKNNVKLTSISALITYIVLTIVLSVFGVLSVLACVLMYKQKQOQKTLWLIG 540

QY	541	NNTL	DQMRA	TTKM	553
				:	
Db	541	NNTL	DQMRA	TTKI	553

RESULT 9
VGNZNV

VGNZNV

cell fusion glycoprotein precursor - Newcastle disease virus (strains Beaudette C and B)
N/Contents: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C/Accession: A27008; F46329
R/Chambers, P.; Millar, N.S.; Emmerson, P.T.
J. Gen. Virol. 67, 2685-2694, 1986
A/Title: Nucleotide sequence of the gene encoding the fusion glycoprotein of Newcastle
A/Reference number: A27008; UID:87085486; PMID:3025345
A/Accession: A27008
A/Molecule type: mRNA
A/Residues: 1-553 <CHA>
A/Cross-references: GB:X04719; NID:G60933; PIDN:CAA28426.1; PID:g60934
A/Experimental source: strain Beaudette C
R/Ioyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generation
A/Reference number: A46329; UID:89204898; PMID:2705298
A/Accession: F46329
A/Molecule type: genomic RNA
A/Residues: 1-553 <TOY>
A/Cross-references: GB:M24697; NID:G293929; PIDN:AAA46648.1; PID:G293930
A/Experimental source: strain BEA/45
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F/118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F/495-528/Domain: transmembrane #status predicted <TMN>
F/85,191,366,447,471/Banding site: carbohydrate (Asn) #status predicted

Query Match	94.4%	Score 2603	DB 1	Length 553
Best Local Similarity	93.5%	Pred. No. 5.2e-155		
Matches 517; Conservative	19	Mismatches 17	Indels 0	Gaps 0

QY	1	MGRSRSTRIPVPLMLTVRVALSCVPTSLDGRPLAAGIVVTGDKAVNIYTSSQTGS	60
Db	1	MGPRESTXNPVPMMLTVRVALVLSCI PFANSIDGRPLAAGIVVTGDKAVNIYTSSQTGS	60

	Qy	Db
61	IVKLLPNPKDKKACAKAPLEAYNRILTTLLPLGDSIRRIQESVTTSGGKGQRUGA	120
61	IVKLLPNLPDKKACAKAPLDAYNRILTTLLPLGDSIRRIQESVTTSGRRKQKPIGA	120

180	QY	180	QY
181	QY	181	QY
182	QY	182	QY
183	QY	183	QY
184	QY	184	QY
185	QY	185	QY
186	QY	186	QY
187	QY	187	QY
188	QY	188	QY
189	QY	189	QY
190	QY	190	QY
191	QY	191	QY
192	QY	192	QY
193	QY	193	QY
194	QY	194	QY
195	QY	195	QY
196	QY	196	QY
197	QY	197	QY
198	QY	198	QY
199	QY	199	QY
200	QY	200	QY

Db	181	KXQGFVNDQFNKTAQELGCGIRIAQQGVENLNYLTETTVFGPQISPAINKLTIQALYN	240
Qy	241	LAGGNWVYLTKLGVNGNOISLISGSLITCNIPILVDSQTOLLGIQVTIPGVGNLNMRA	300

db 241 LAGGMDYLLTKLGVGNQLSSLIGSLITGNPILYDSQTQLLIGIQVTLPSVGNLNNMEA 300

QY 301 TYLTSLVSSTTKGPASALVPQVMKGVIEELDTSYCIETDLDLIXCTRITFPMPSPGIY 360

301 TYLETSVSTRGPASALVPKVTQGVSVIEELDTSCYETDLDTCTRIIVTFPMSPGY 360

361 SCLSGNTSACWYSKTEGALTTPYMLTKGSVIANCKMTTCRADPPGIIISONGYEAUSLID 420

421	ROSCNVLSLDGITURLSGEFDATYQKNISIQDSQSVITVGNLDDISTELGNVNNSISNALDK	480
361	SCLSGNTSACMYSKIEGALTTPYMIIRKGSVIANCKMTTCRCVNPPIISQNYGEAVSLID	420

Db 421 KQCNVLSLGGITLRLSGEFATYQKNISIQDSQVITGMDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 10

S40163
cell fusion protein - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S40163
R:Kalinan, A.; Zadori, Z.; Kisari, J.; Fodor, I.
submitted to the EMBL Data Library, May 1993
A:Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) gene of newca
A:Reference number: S40163
A:Accession: S40163
A:Status: Preliminary
A:Molecule type: genomic RNA
A:Residues: 1-553 <KAL>
A:Cross-references: EMBL:X71995; NID:9437886; PIDN:CAAS0869.1; PID:9437887
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 94.4%; Score 2602; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 6e-155;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGRSSSTRIPVPLMTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MRSRSSTRIPVPLMTIRIALTLSCIRLTSSLDGRPLTAAGIVVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGRRQRFIGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQANQNAANILRLKESIAATNEAAHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTIQALYN 240
Qy 241 LAGNMDVLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGILQITLPSVGNLNNMRA 300
Db 241 LAGNMDVLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGILQITLPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Qy 421 ROSCNVLSLDGITLRLSGEFATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFATYQKNISILDSQVIVTGNLDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 12

RESULT 11

S06345

cell fusion glycoprotein precursor - Newcastle disease virus (strain Italian)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 24-Nov-1999
C:Accession: S06345
R:Espion, D.; de Henau, S.; Letellier, C.; Wemmers, C.D.; Brasseur, R.; Young, J.F.; Gros
Arch. Virol. 95, 79-95, 1987
A:Title: Expression at the cell surface of native fusion protein of the Newcastle disease
A:Reference number: S06345; MUID:87240797; PMID:3592986
A:Accession: S06345
A:Molecule type: Genomic RNA
A:Residues: 1-553 <ESP>
A:Cross-references: EMBL:M17710
A:Note: it is uncertain whether Met-1 or Met-14 is the initiator
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-116/Product: fusion glycoprotein F2 #status predicted <F2P>
F:117-553/Product: fusion glycoprotein F1 #status predicted <F1P>
F:495-525/Domain: transmembrane #status predicted <TM>
F:85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.3%; Score 2599; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 9.2e-155;
Matches 522; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMTVRVALALSCVPTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Db 1 MRSRSSTRIPVPLMTIRIALTLSCIRLTSSLDGRPLAAAGIVVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQSVTTSGGRRQRFIGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATAAQITTAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQGVGVELNLYLTTELTVFGPQITSPALTIQALYN 240
Qy 241 LAGNMDVLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGILQITLPSVGNLNNMRA 300
Db 241 LAGNMDVLLTKLGVGNQLSSLGSLITGNPILYDSQTQLGILQITLPSVGNLNNMRA 300
Qy 301 TYLETSLVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETSLVSTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
Qy 421 ROSCNVLSLDGITLRLSGEFATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db 421 RHSCNVLSLDGITLRLSGEFATYQKNISILDSQVIVTGNLDISTELGNVNSISNALNK 480
Qy 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSLITYIVLTIVLSVCGILSLVACLYMYKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

A36830

cell fusion glycoprotein precursor - Newcastle disease virus (strain HER/33)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2

C;Species: Newcastle disease virus

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C;Accession: A36830

R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virology 169, 273-282, 1989

A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A;Reference number: A46329; MUID:89204899; PMID:2705298

A;Accession: A36830

A;Molecule type: genomic RNA

A;Residues: 1-553 <TOY>

A;Cross-references: GB:M24702; NID:g293937; PIDN:AAA46652.1; PID:g293938

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F;118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>

F;495-528/Domain: transmembrane #status predicted <TMN>

F;85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 94.2%; Score 2598; DB 1; Length 553;

Best Local Similarity 94.4%; Pred. No. 1.1e-154;

Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60

DB 1 MGRSRSTRIPVPPMLIIRIVLTLSCLIRLTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGGHQLRIGA 120

DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGRRQRRFIGA 120

QY 121 IIGGAALGVATAACITTAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180

DB 121 IIGSVALGVATAAQITTAASALIQANQANANILRLKESIAATNEAVHEVTDGLSOLAVAG 180

QY 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETLTVFGPQITSPALTIQALYN 240

DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETLTVFGPQITSPALTIQALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

DB 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

DB 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420

DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420

QY 421 ROSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480

DB 421 RHSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLAMYKOKAQKTLWLWG 540

DB 481 LEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLAMYKOKAQKTLWLWG 540

QY 541 NNTLDQMRATTM 553

DB 541 NNTLDQMRATTM 553

RESULT 13

G46329

cell fusion glycoprotein precursor - Newcastle disease virus (strain TEX/48)

N;Contains: fusion glycoprotein F1; fusion glycoprotein F2

C;Species: Newcastle disease virus

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C;Accession: G46329; S11266

R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virology 169, 273-282, 1989

A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A;Reference number: A46329; MUID:89204899; PMID:2705298

A;Accession: G46329

A;Molecule type: genomic RNA

A;Residues: 1-553 <TOY>

A;Cross-references: GB:M24698; NID:g293931; PIDN:AAA46649.1; PID:g293932

R;Richardson, C.D.; Scheid, A.; Chopin, P.W.

Virology 105, 205-222, 1980

A;Title: Specific inhibition of paramyxovirus and myxovirus replication by oligopeptide:

A;Reference number: S11266; MUID:81016739; PMID:7414950

A;Accession: S11266

A;Molecule type: protein

A;Residues: 117-136 <RIC>

C;Genetics:

A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein

C;Keywords: glycoprotein; membrane fusion; transmembrane protein

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F;118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>

F;495-528/Domain: transmembrane #status predicted <TMN>

F;85,191,366,447,471/Binding site: carbohydrate (Asn) #status predicted

Query Match 94.1%; Score 2593; DB 1; Length 553;

Best Local Similarity 93.1%; Pred. No. 2.2e-154;

Matches 535; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60

DB 1 MGRSRSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS 60

QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGGHQLRIGA 120

DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGRRQRRFIGA 120

QY 121 IIGGAALGVATAACITTAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAG 180

DB 121 IIGSVALGVATAAQITTAASALIQANQANANILRLKESIAATNEAVHEVTDGLSOLAVAG 180

QY 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETLTVFGPQITSPALTIQALYN 240

DB 181 KMQQFVNDQFNNTAQELDCIKITQQVGVVELNLYLTETLTVFGPQITSPALTIQALYN 240

QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

DB 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

DB 301 TYLETLSVTTKGFASALVPKVMKGVSVIEELDTSCYIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420

DB 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420

QY 421 ROSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480

DB 421 KQSCNVSLDGLTIRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLAMYKOKAQKTLWLWG 540

DB 481 LEESNSKLDKVNKLTSTSAITYIVLTIVSLVCGILSLVLACYLAMYKOKAQKTLWLWG 540

QY 541 NNTLDQMRATTM 553

DB 541 NNTLDQMRATTM 553

RESULT 14

B36930
cell fusion glycoprotein precursor - Newcastle disease virus (strain ITA/45)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Accession: B36930
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
R;Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.; D
A;Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neurot
Virology 169, 273-285, 1989
C;Accession: B36830
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: B36830
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: Glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;117-117/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;495-528/Domain: transmembrane #status predicted <TMN>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.0%; Score 2592; DB 1; Length 553;
Best Local Similarity 94.2%; Pred. No. 2.5e-154; Mismatches 20; Indels 0; Gaps 0;
Matches 521; Conservative 12; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
Db 1 MRSRSSTRIPVPLMLIIRIALTSLIRLTSSLDGRPLAAAGIVTGDKAVDIYTSSTQGS 60
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGRRKRFIGA 120
Qy 121 IIGGALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGSVLGVATPAQITAAALIQANNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOALYN 240
Db 181 KMOQFVNDQFNNTAQQLDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOALYN 240
Qy 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Qy 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID 420
Qy 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 RHCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKAAQKTLWLIG 540
Db 481 LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKAAQKTLWLIG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553

RESULT 15

VANZGB
cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas G.B.)

N;Contains: fusion glycoprotein F1; fusion glycoprotein F2

C;Species: Newcastle disease virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: B29201
R;Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.; D
A;Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neurot
Virology 165, 291-295, 1988
C;Accession: B29201
A;Reference number: A94379; MUID:88265873; PMID:3388773

A;Molecule type: mRNA
A;Residues: 1-553 <SCH>
A;Experimental source: strain Texas G.B.
C;Genetics:
A;Gene: F

C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: Glycoprotein; membrane fusion; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-111/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F;112-116/Product: cleavage processing #status predicted
F;117-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;9,85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.9%; Score 2589; DB 1; Length 553;
Best Local Similarity 92.9%; Pred. No. 3.9e-154;
Matches 514; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
Db 1 MGRPSPTKPTPMLTVRVALVLGICIPANSIDGRPLAAAGIVTGDKAVNIYTSSTQGS 60
Qy 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGRKRFIGA 120
Qy 121 IIGGALGVATAAQITAAALIQANNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGVALGVATAAQITAAALIQAKNAANILRLKESIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTETTVFGPQITSPALTLTIOALYN 240
Db 181 KMOQFVNDQFNKTAQESGIRIAQOVGVNELNLYLTETTVFGPQITSPALNKLTIQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Db 241 LAGNMDYLLTKLGVGNQLSSLGSLITGNPILYDSOTQLLGIQVTLPSVGNLNMRA 300
Qy 301 TYLETLVSSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLVSSTTRGFASALVPKVVTVQGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGAVSLID 420
Db 361 SCLSGNTSACMYKTEGALTTPYMTIRKSVIANCKMTTCRCVNPFGIISQNYGAVSLID 420
Qy 421 RQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
Db 421 KQSCNVLSLGGITLRLSGEFDATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
Qy 481 LEESNKLDKVNVKLTSTALITYIVLTIVSLVCGILSLVACVLMYKQKAAQKTLWLIG 540
Db 481 LEESNKLDKVNVKLTSTALITYIVLTIVSLVFGILSLVACVLMYKQKAAQKTLWLIG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

Search completed: April 18, 2004, 02:33:33
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: April 18, 2004, 01:19:18 ; Search time 46 Seconds
(without alignments)
1156.389 Million cell updates/sec

Title: US-10-725-841-2
Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRVA.....KTLWLGNLTLDQMRATTKM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2724	98.8	553	1 VGNZU1	cell fusion glycop
2	2724	98.8	553	1 A46329	cell fusion glycop
3	2691	97.6	553	2 S23621	gene F protein - N
4	2684	97.4	553	1 B46329	cell fusion glycop
5	2658	96.4	553	2 S38785	gene F protein - N
6	2625	95.2	553	1 H46329	cell fusion glycop
7	2622	95.1	553	1 D46329	cell fusion glycop
8	2606	94.5	553	1 VGNZTE	cell fusion glycop
9	2603	94.4	553	1 VGNZNV	cell fusion glycop
10	2602	94.4	553	2 S40163	cell fusion glycop
11	2599	94.3	553	2 S06345	cell fusion glycop
12	2598	94.2	553	1 A36830	cell fusion glycop
13	2593	94.1	553	1 A36830	cell fusion glycop
14	2592	94.0	553	1 B36830	cell fusion glycop
15	2589	93.9	553	1 VGNZGB	cell fusion glycop
16	2588	93.9	553	1 B46329	cell fusion glycop
17	2585	93.8	553	1 I46329	cell fusion glycop
18	2579	93.5	553	1 VGNZND	cell fusion glycop
19	2575	93.4	553	2 S38784	gene F protein - N
20	2555	92.7	553	2 S23622	gene F protein - N
21	2554	92.6	553	2 S23620	F protein - N
22	2549	92.5	553	2 S38786	gene F protein - N
23	1018.5	36.9	534	2 A37483	F protein - Muraya
24	717	26.0	529	1 VGNZSP	cell fusion glycop
25	712.5	25.8	538	1 VGNZMM	cell fusion glycop
26	712.5	25.8	538	2 S52472	cell fusion glycop
27	704	25.5	538	1 VGNZMS	cell fusion glycop
28	704	25.5	551	1 VGNZP2	cell fusion glycop
29	701.5	25.4	538	1 VGNZMU	cell fusion glycop

30	701	25.4	551	1 VGNZPG	cell fusion glycop
31	691	25.1	538	1 B60004	cell fusion glycop
32	671	24.3	561	1 VGNZ41	cell fusion glycop
33	638.5	23.2	542	2 JQ2223	cell fusion protei
34	636	23.1	631	1 VGNZPD	cell fusion glycop
35	636	23.1	631	1 A48346	cell fusion glycop
36	631	22.9	546	2 S47300	gene F protein - r
37	624.5	22.7	662	2 S21382	cell fusion glycop
38	621.5	22.5	662	1 VGNZCD	cell fusion glycop
39	610.5	22.1	550	1 E48556	cell fusion glycop
40	610	22.1	636	2 S47299	gene F protein - r
41	608.5	22.1	546	1 VGNZRL	cell fusion glycop
42	605.5	22.0	553	1 VGNZMV	cell fusion glycop
43	603.5	21.9	546	1 VGNZRK	cell fusion glycop
44	599.5	21.7	546	2 S47305	gene F protein - r
45	596.5	21.6	552	2 S47034	cell fusion protei

ALIGNMENTS

RESULT 1

VGNZU1
cell fusion glycoprotein precursor - Newcastle disease virus (strains Ulster and ULS/e
N; Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C:Accession: A29823; C46329
R:Millar, N.S.; Chambers, P.; Emerson, P.T.
J. Gen. Virol. 69, 613-620, 1988
A:Title: Nucleotide sequence of the fusion and haemagglutinin-neuraminidase glycoprote
ns.
A:Reference number: A92799; MUID:88171450; PMID:3351479
A:Accession: A29823
A:Molecule type: mRNA
A:Residues: 1-553 <MIL>
A:Cross-references: GB:D00243; NID:G222174; PIDN:BA00173.1; PID:G222175
A:Experimental source: strain Ulster
R:Toyoda, T.; Sakauchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virolgy 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generati
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: C46329
A:Molecule type: genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24694; NID:G293923; PIDN:AAA46645.1; PID:G293924
A:Experimental source: strain ULS/67
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;
Best Local Similarity 99.1%; Pred. No. 1.4e-162;
Matches 548; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MGRSSTRIPVPLMLTVRVALSCVPTSLDGRPLAAAGIVVTGKAVNIYTSQTGS	60
Db	1	MGRSSTRIPVPLMLTVRVALSCVPTSLDGRPLAAAGIVVTGKAVNIYTSQTGS	60
Qy	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA	120
Db	61	IIVKLLPNMPKDEACAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA	120
Qy	121	IIGGALGVATAAQITAAASALIOANQNAANILRKERIAATNEAVHEVTDGLSOLAVAVG	180
Db	121	IIGGALGVATAAQITAAASALILANQNAANILRKESIAATNEAVHEVTDGLSOLAVAVG	180

QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 421 RQSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 421 RQSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 481 LEESNSKLDKVNKLTSTTSALITYIVLTIVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 481 LEESNSKLDKVNKLTSTTSALITYIVLTIVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||

RESULT 2

A46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain D26/76)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A46329
R:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A:Reference number: A46329; PMID:2705298
A:Accession: A46329
A:Molecule type: Genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24692; NID:G293919; PIDN:AAA46643.1; PID:G293920
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: Glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F126-117/Product: cell fusion glycoprotein F2 #status predicted <PF2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <PF1>
F495-528/Domain: transmembrane #status predicted <TMN>
F185,191,366,447,471/Binding site: carbohydrate (asn) #status predicted

Query Match 98.8%; Score 2724; DB 1; Length 553;
Best Local Similarity 98.4%; Pred. No. 1.4e-162;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
DB |||||
QY 1 MGSRSSTRIPVPLMLTVRIMALSVCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANILRLKERIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 121 IIGGVALGVATAAQITAAALIOANQANILRLKESIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||

QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||
QY 421 RQSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 421 RQSCNVLSLDGTTILRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
DB |||||
QY 481 LEESNSKLDKVNKLTSTTSALITYIVLTIVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 481 LEESNSKLDKVNKLTSTTSALITYIVLTIVISLVCGLISLVACYLKYKAKOQKTLMLG 540
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||
QY 541 NNTLDQMRATTKM 553
DB |||||

RESULT 3

S23621
gene F protein - Newcastle disease virus
C:Species: Newcastle disease virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 25-Oct-1996
C:Accession: S23621
R:Pritzer, E.; Kuroda, K.; Garten, W.; Nagai, Y.; Klenk, H.D.
Virus Res. 15, 237-242, 1990
A:Title: A host range mutant of Newcastle disease virus with an altered cleavage site
A:Reference number: S23620; PMID:90261333; PMID:2188464
A:Accession: S23621
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-553 <PRI>
A:Cross-references: EMBL:Z12110
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 97.6%; Score 2691; DB 2; Length 553;
Best Local Similarity 98.2%; Pred. No. 1.7e-160;
Matches 543; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
DB |||||
QY 1 MGSRSSTRIPVPLMLTVRVALSVCVPTSSLDGRPLAAAGIVVTGDKAVNIYTSSQTS 60
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTTLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANILRLKERIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 121 IIGGAALGVATAAQITAAALIOANQANILRLKESIAATNEAVEHVTGSLQAVAVG 180
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||
QY 181 KMQQFVNDQFNKTAQELDCIKITQGVVELNLYLTETLVFGPQITSPALQTQITQALYN 240
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNPILYDSQTOLLGIVTLPSPVGNLNNMRA 300
DB |||||
QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 301 TYLETLSVSTTKGFASARVPKVVTVQVSGVIGELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
DB |||||
QY 361 SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
DB |||||

Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
Db 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 4
B46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain Que/66)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: B46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24693; NID:g293921; PIDN:AAA46644.1; PID:g293922
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TM>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.4%; Score 2684; DB 1; Length 553;
Best Local Similarity 97.3%; Pred. No. 4.5e-160;
Matches 538; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMOQFVNDQNKTAOELDCIKITQOVGVLENLYLTTLTTPGDSIRRIQESVTTSGGKQGRLLGA 240
Db 181 KMOQFVNDQNKTAOELDCIKITQOVGVLENLYLTTLTTPGDSIRRIQESVTTSGGKQGRLLGA 240
QY 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLDTXTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLDTXTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
Db 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
Db 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 5
S38785
Gene F protein - Newcastle disease virus
C:Species: Newcastle disease virus
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S38785
R;Garten, W.D.
submitted to the EMBL Data Library, May 1992
A;Reference number: S22083
A;Accession: S38785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-553 <GAR>
A;Cross-references: EMBL:Z12110; NID:g60658; PIDN:CAA78095.1; PID:g60659
C;Superfamily: parainfluenza virus cell fusion protein

Query Match 96.4%; Score 2658; DB 2; Length 553;
Best Local Similarity 96.9%; Pred. No. 1.9e-158;
Matches 536; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
Db 1 MGSRSSTRIPVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKKACAKAPLEAYNRTLTLLTPGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMOQFVNDQNKTAOELDCIKITQOVGVLENLYLTTLTTPGDSIRRIQESVTTSGGKQGRLLGA 240
Db 181 KMOQFVNDQNKTAOELDCIKITQOVGVLENLYLTTLTTPGDSIRRIQESVTTSGGKQGRLLGA 240
QY 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNDYLLTKLGVGNQNLSSGLITGNPILYDSQTLGLGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLDTXTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYIEFDLDTXTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSTEGALTPPYMTLKGSVIANCKMTTCRCADPPGLISQNYGEAVSLID 420
QY 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVSLDGIITRLSGEFDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
QY 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
Db 481 LEESNKLKDVNVKLTSTSTALITYIVLTIVISLVCGILSLVLACVLMYKQKAAQKTLILWG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 6

H46329

N:Contains: fusion glycoprotein precursor - Newcastle disease virus

C:Species: fusion glycoprotein F1; fusion glycoprotein F2

C>Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: S07422; H46329

R:McGinnes, L.W.; Morrison, T.G.

Virus Res. 5, 343-356, 1986

A:Title: Nucleotide sequence of the gene encoding the Newcastle disease virus fusion protein

A:Reference number: S07422; MUID:87044526; PMID:3776349

A:Accession: S07422

A:Molecule type: mRNA

A:Residues: 1-553 <MCG>

A:Cross-references: EMBL:M21881

A:Experimental source: strain Australia-Victoria

R:Toyoda, T.; Sakeguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.

Virology 169, 273-282, 1989

A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating

A:Reference number: A46329; MUID:89204898; PMID:2705298

A:Accession: H46329

A:Molecule type: genomic RNA

A:Residues: 1-65, 'H', 67-553 <TOY>

A:Cross-references: GB:M24700; NID:G293933; PIDN:AAA46650.1; PID:G293934

A:Experimental source: strain AUS/32

C:Genetics:

A:Gene: F

C:Superfamily: parainfluenza virus cell fusion protein

C:Keywords: glycoprotein; membrane fusion; transmembrane protein

F#1-25/Domain: signal sequence #status predicted <SIG>

F#25-116/Product: cell fusion glycoprotein F2 #status predicted <PF2>

F#112-116/Region: cleavage processing #status predicted

F#117-553/Product: cell fusion glycoprotein F1 #status experimental <PF1>

F#499-526/Domain: transmembrane #status predicted <TMN>

F#85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

F#85,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.2%; Score 2625; DB 1; Length 553;

Best Local Similarity 95.5%; Pred. No. 2.2e-156;

Matches 528; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MGSRSTRIPVPLMLTVRVALALSCVPTSLDGRPLAAAAGIVVTGKAVNIYTSQTGS	60
Dd	1	MGPRSSTRIPPLMLTRIALALSCVHLASSDLGRPLAAAAGIVVTGDKAVNIYTSQTGS	60
Qy	61	IIIVKLLPNMPKDEACAKAPLEAVNRTLTTLLPLGDSIRRIQESVTTSGGKQGRLIGA	120
Dd	61	IIIVKLLPNMPKDEACAKAPLEAVNRTLTTLLPLGDSIRRIQESVTTSGRRQKRFIGA	120
Qy	121	IIIGSALGVATAAQITAAASALIQANQANAILRLKERIAATNEAVHVTVDGLSOLAVAVG	180
Dd	121	IIIGSALGVATAAQITAAASALIQANQANAILRKESITATIEAVHVTVDGLSOLAVAVG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQQGVNELNLYITELTTVFGPQITSPALTTQTITQALYN	240
Dd	181	KMQQFVNDQFNNTAQELDCIKITQQGVNELNLYITELTTVFGPQITSPALTTQTITQALYN	240
Qy	241	LAGNMNDYLLTKLGVGNQNLSSLIGSLITGNPLIYDSOTQLAGIQTVLPSVGNLNMRA	300
Dd	241	LAGNMNDYLLTKLGVGNQNLSSLIGSLITGNPLIYDSOTQLAGIQTVLPSVGNLNMRA	300
Qy	301	TYLETLSVSTTKGFASALPVKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFFMSPGIY	360
Dd	301	TYLETLSVSTTKGFASALPVKVVTVQVSGVIEELDTSYCIETDLDLYCTRIVTFFMSPGIY	360
Qy	361	SLCSGNTSACMYSKXTEGALTPPYMLTKGSVIANKCKMTTCRCADPPGIISQNYGEAVSLID	420
Dd	361	SLCNGNTSACMYSKXTEGALTPPYMLTKGSVIANKCKMTTCRCADPPGIISQNYGEAVSLID	420
Qy	421	RQSCNVLSLDGITILRLSGEPDATYQKNISIQDSQVITVGNLDTSTELGNVNNNISNALDK	480
Dd	421	RHSNCNVLSLDGITILRLSGEPDATYQKNISITLDSQVITVGNLDTSTELGNVNNNISNALDK	480

```

Qy 481 LEENSKLDKNVKLTSTSTALITYIVLTVISLVCGLISLVACYLWYKQAKOQKILLWLG 540
Db 481 LEENSKLDKNVKLTSTSTALITYIVLTVISLVCGLISLVACYLWYKQAKOQKILLWLG 540
Qy 541 NNTILDQWRATTKM 553
Db 541 NNTILDQWRATTKM 553

RESULT 7
D46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain BI/47)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: D46329
E:Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagao
Virology 169, 273-282, 1989
A:Title: Newcastle disease virus evolution. II. Lack of gene recombination in
A:Reference number: A46329; MUID:89204898; PMID:2705298
A:Accession: D46329
A:Molecule type: genomic RNA
A:Residues: 1-553 <TOY>
A:Cross-references: GB:M24695; NID:G293925; PIDN:AAA46646.1; PID:G293926
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predi
Query Match 95.1%; Score 2622; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 3.4e-156;
Matches 517; Conservative 21; Mismatches 15; Indels 0; Gaps 0

```

Qy	1	MGSRSTRIPVPLMLTVRVVALASCVCPTSSLDGRPLAAAGIVTGDKAVNIYTSQTGS	60
Db	1	MGSRPSTKIPAPMMLTRIVALLVLSICIPANSIDGRPLAAAGIVTGDKAVNIYTSQTGS	60
Qy	61	IIIVKLLPNMPKDEACAKAPLEAYNRILTLLTPLGDSIRRIQESVTTSGGKGQRLLGA	120
Db	61	IIIVKLLPNLPDKDEACAKAPUDAYNRILTLLTPLGDSIRRIQESVTTSGGKGQRLLGA	120
Qy	121	IIIGGALGVATAAQITTAASALIQANQANANILRLKERIAATNEAVEHTDGLSQLAVAG	180
Db	121	IIIGGALGVATAAQITTAASALIQAKQANANILRLKESIAATNEAVEHTDGLSQLAVAG	180
Qy	181	KMQQFVNDQFNKTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALQTOLTQALYN	240
Db	181	KMQQFVNDQFNKTAQELDCIKIAQQGVVELNLYLTETLTVFGPQITSPALNKLTQALYN	240
Qy	241	LAGNNMYLLTKLGVGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Db	241	LAGNNMYLLTKLGIIGNQNLSSLGSLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRA	300
Qy	301	TYLBTLSVSTTKGFASALPVKVMKVGSVIBELDTSYCIETDLDLYCYTRIVTFPMSPGY	360
Db	301	TYLBTLSVSTRGFASALPVKVTQVGSVIBELDTSYCIETDLDLYCYTRIVTFPMSPGY	360
Qy	361	SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKWMTTCRCADPPGIIISQNYGEAVSLID	420
Db	361	SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKWMTTCRCVNPFGIIISQNYGEAVSLID	420
Qy	421	RQSCNVLSLDGIIURLGSEPDATYQKNISIODSOVITGNLIDISTELGNVNNISNALDK	480
Db	421	KQSCNVLSLGGIURLGSEPDVTVQKNISIODSVIITGNLIDISTELGNVNNISNALNK	480
Qy	481	LEESNRKLDKVNKLTSTALITYIVLTIVLSLVGCGILSVLIACYLMTYKQKAAQKTLWIG	540
Db	481	LEESNRKLDKVNKLTSTALITYIVLTIVLSLVGCGILSVLIACYLMTYKQKAAQKTLWIG	540

QY 541 NNTLDMQRAATTKM 553
Db |||||
541 NNTLDMQRAATTKI 553

RESULT 8

VGNZNV

cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A34663
R;Taylor, J.; Edbauer, C.; Rey-Senelange, A.; Bouquet, J.F.; Norton, E.; Goebel, S.; Des
J. Virol. 64, 1441-1450, 1990
A;Title: Newcastle disease virus fusion protein expressed in a fowlpox virus recombinant
A;Reference number: A34663; MUID:90204652; PMID:2157037
A;Accession: A34663
A;Molecule type: genomic RNA
A;Residues: 1-553 <TAY>
A;Cross-references: EMBL:M33855; NID:9332369; PIDN:AAA46675.1; PID:9332370
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;112-116/Region: cleavage processing #status predicted <FF2>
F;117-553/Product: cell fusion glycoprotein F1 #status predicted <TMI>
F;117-133/Domain: transmembrane #status predicted <TM1>
F;504-521/Domain: transmembrane #status predicted <TM2>
F;85-131,366,447,471,541/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 94.5%; Score 2606; DB 1; Length 553;
Best Local Similarity 94.8%; Pred. No. 3.4e-155;
Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSRTPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNYITSSOTGS 60
Db |||||
1 MGRSSRTPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNYITSSOTGS 60
QY 61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVITSGGKQRLIGA 120
Db |||||
61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVITSGGKQRLIGA 120
QY 121 IIGGALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db |||||
121 IIGGALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
Db |||||
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
Db |||||
241 LAGNMDYLLTKLGVGNQNSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVKVGVSVIEELDTSCYIEDLDTCTRIIVTFPMSGIY 360
Db |||||
301 TYLETSLVSTTKGFASALVPKVKVGVSVIEELDTSCYIEDLDTCTRIIVTFPMSGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db |||||
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
Db |||||
421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480
QY 481 LEENSKLDKVNKLTSTSLITVILTVISLVGILSLVACIMYKQKQKTLWLW 540
Db |||||
481 LEENSKLDKVNKLTSTSLITVILTVISLVGILSLVACIMYKQKQKTLWLW 540

QY 541 NNTLDMQRAATTKM 553
Db |||||
541 NNTLDMQRAATTKI 553

RESULT 9

VGNZNV

cell fusion glycoprotein precursor - Newcastle disease virus (strains Beaudette C and
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C;Accession: A27008; F46329
R;Chambers, P.; Millar, N.S.; Emmerson, P.T.
J. Gen. Virol. 67, 2685-2694, 1986
A;Title: Nucleotide sequence of the gene encoding the fusion glycoprotein of Newcastle
A;Reference number: A27008; MUID:87085486; PMID:3025345
A;Accession: A27008
A;Molecule type: mRNA
A;Residues: 1-553 <CHA>
A;Cross-references: GB:X04719; NID:G60933; PIDN:CAA28426.1; PID:G60934
A;Experimental source: strain Beaudette C
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generati
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: F46329
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24697; NID:G293929; PIDN:AAA46648.1; PID:G293930
A;Experimental source: strain BEA/45
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;495-528/Domain: transmembrane #status predicted <TMN>
F;85-131,366,447,471/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 94.4%; Score 2603; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 5.2e-155;
Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSRTPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNYITSSOTGS 60
Db |||||
1 MGRSSRTPIVPLMLTVRVVALALSCVPTSSLDGRPLAAGIVTGDKAVNYITSSOTGS 60
QY 61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVITSGGKQRLIGA 120
Db |||||
61 IIVKLLPNMPKDKKAKAPLEAYNRTLTLLTPLGDSIRRIQESVITSGGKQRLIGA 120
QY 121 IIGGALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db |||||
121 IIGGALGVATAAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
Db |||||
181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTVPQITSPALTIQALYN 240
QY 241 LAGNMDYLLTKLGVGNQNSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
Db |||||
241 LAGNMDYLLTKLGVGNQNSLIGSLITGNPILYDSQTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETSLVSTTKGFASALVPKVKVGVSVIEELDTSCYIEDLDTCTRIIVTFPMSGIY 360
Db |||||
301 TYLETSLVSTTKGFASALVPKVKVGVSVIEELDTSCYIEDLDTCTRIIVTFPMSGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIIISQNGEAVSLID 420
Db |||||
361 SCLSGNTSACMYSKTEGALTTPYMTLKGSIANCKMTTCRCADPPGIIISQNGEAVSLID 420
QY 421 ROSCNVSLDGIITRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNSISNALDK 480

Db 421 :|||||KSCNVLSLGGITRLSGFDATYQKNIISIQDSQVITGTLNDISTELGNVNNISNALNK 480
QY 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
Db 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 10

S40163
cell fusion protein - Newcastle disease virus
C:Species: Newcastle disease virus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S40163
R:Kallman, A.; Zadori, Z.; Kieari, J.; Podor, I.
submitted to the EMBL Data Library, May 1993
A:Description: Nucleotide sequence of the hemagglutinin-neuraminidase (HN) gene of newca
A:Reference number: S40163
A:Accession: S40163
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-553 <NAL>
A:Cross-references: EMBL:X71995; NID:g437886; PIDN:CAA50869.1; PID:g437887
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 94.4%; Score 2602; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 6e-155;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVVALSVCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
Db 1 MGRSSTRIPVPLMLIIRIALTSLCIRLTSSLDGRPLTAAAGIVTGDKAVNIYTSQTS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQKRLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGRRQRFIGA 120
QY 121 IIGGALGVATAAQTAAASALIOANONANILRLKERIAATNEAHEVTDGLSOLAVAG 180
Db 121 IIGSVALGVATAAQTAAASALIOANONANILRLKESIAATNEAHEVTDGLSOLAMAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLVFGPQITSPALTTIQAALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNYLTETLVFGPQITSPALTTIQAALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQNLSSIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMALKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITRLSGFDATYQKNIISIQDSQVITGTLNDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLGGITRLSGFDATYQKNIISILDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
Db 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

RESULT 12

RESULT 11
S06345
cell fusion glycoprotein precursor - Newcastle disease virus (strain Italian)
N:Contains: fusion glycoprotein F1; fusion glycoprotein F2
C:Species: Newcastle disease virus
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 24-Nov-1999
C:Accession: S06345
R:Espion, D.; de Henau, S.; Letellier, C.; Wemmers, C.D.; Brasseur, R.; Young, J.F.; Gr
Arch. Virol. 95: 79-95, 1987
A:Title: Expression at the cell surface of native fusion protein of the Newcastle dise
A:Reference number: S06345; MUID:87240797; PMID:3592986
A:Accession: S06345
A:Molecule type: genomic RNA
A:Residues: 1-553 <ESP>
A:Cross-references: EMBL:M17710
A:Note: It is uncertain whether Met-1 or Met-14 is the initiator
C:Genetics:
A:Gene: F
C:Superfamily: parainfluenza virus cell fusion protein
C:Keywords: glycoprotein; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-116/Product: fusion glycoprotein F2 #status predicted <F2P>
F:117-553/Product: fusion glycoprotein F1 #status predicted <F1P>
F:495-525/Domain: transmembrane #status predicted <TM>
F:185,191,366,447,471,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 94.3%; Score 2599; DB 2; Length 553;
Best Local Similarity 94.4%; Pred. No. 9.2e-155;
Matches 522; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
QY 1 MGRSSTRIPVPLMLTVRVVALSVCVPTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
Db 1 MGRSSTRIPVPLMLIIRIALTSLCIRLTSSLDGRPLAAAGIVTGDKAVNIYTSQTS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGKQKRLIGA 120
Db 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLTLPGLDSIRRIQESVTTSGGRRQRFIGA 120
QY 121 IIGGALGVATAAQTAAASALIOANONANILRLKERIAATNEAHEVTDGLSOLAVAG 180
Db 121 IIGSVALGVATAAQTAAASALIOANONANILRLKESIAATNEAHEVTDGLSOLAVAG 180
QY 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNYLTETLVFGPQITSPALTTIQAALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQVGVNELNYLTETLVFGPQITSPALTTIQAALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLGVGNQNLSSIGSLITGNPILYDSQTLGLIGQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSYKTEGALTTPYMALKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLGGITRLSGFDATYQKNIISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RHSCNVLSLGGITRLSGFDATYQKNIISILDSQVIVTGNLIDISTELGNVNNISNALNK 480
QY 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
Db 481 LLEESNKLKDNVNLKSTALITYIVLVTVISLVCGILSLVLAACYLVMYKQKQKQKTLMLG 540
QY 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553

A36830
cell fusion glycoprotein precursor - Newcastle disease virus (strain HRR/33)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2
C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C/Accession: A36830
R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virolgy 169, 273-282, 1989
A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A46329; MUID:89204898; PMID:2705298
A/Molecule type: genomic RNA
A/Residues: 1-553 <TOY>
A/Cross-references: GB:M24702; NID:G293937; PIDN:AAA46652.1; PID:G293938
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 94.2%; Score 2598; DB 1; Length 553;
Best Local Similarity 94.4%; Pred. No. 1.1e-154; Mismatches 20; Indels 0; Gaps 0;
Matches 522; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
Db 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMPKDKACAKAPLEAVNRTLTLLTPGDSIRRIQBSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKACAKAPLEAVNRTLTLLTPGDSIRRIQBSVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLQTLQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLQTLQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTLIGTQVLPSPVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTLIGTQVLPSPVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVVQVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVVQVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGTLRLSGEFDATYQKNISIDQSVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGTLRLSGEFDATYQKNISIDQSVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVSLVCGILSLVLACILMYKQKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVSLVCGILSLVLACILMYKQKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKI 553
RESULT 13
G46329
cell fusion glycoprotein precursor - Newcastle disease virus (strain TEX/48)
N/Contains: fusion glycoprotein F1; fusion glycoprotein F2

C/Species: Newcastle disease virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C/Accession: G46329; S11266
R/Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virolgy 169, 273-282, 1989
A/Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A/Reference number: A46329; MUID:89204898; PMID:2705298
A/Accession: G46329
A/Molecule type: genomic RNA
A/Residues: 1-553 <TOY>
A/Cross-references: GB:M24698; NID:G293931; PIDN:AAA46649.1; PID:G293932
R/Richardson, C.D.; Scheid, A.; Choppin, P.W.
Virolgy 105, 205-222, 1980
A/Title: Specific inhibition of paramyxovirus and myxovirus replication by oligopeptid
A/Reference number: S11266; MUID:81016739; PMID:7414950
A/Accession: S11266
A/Molecule type: protein
A/Residues: 117-136 <RIC>
C/Genetics:
A/Gene: F
C/Superfamily: parainfluenza virus cell fusion protein
C/Keywords: glycoprotein; membrane fusion; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-117/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F:118-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F:495-528/Domain: transmembrane #status predicted <TMN>
F:85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 94.1%; Score 2593; DB 1; Length 553;
Best Local Similarity 93.1%; Pred. No. 2.2e-154; Mismatches 19; Indels 0; Gaps 0;
Matches 515; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
Qy 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
Db 1 MGRSSRTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVTGDKAVNIYSSQTGS 60
Qy 61 IIVKLLPNMPKDKACAKAPLEAVNRTLTLLTPGDSIRRIQBSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDKACAKAPLEAVNRTLTLLTPGDSIRRIQBSVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITAAALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Db 121 IIGGAALGVATAAQITAAALIQANQANILRLKERIAATNEAVHEVTDGLSOLAVAG 180
Qy 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLQTLQALYN 240
Db 181 KMQQFVNDQFNNTAQELDCIKITQQGVVELNLYLTETLTVFGPQITSPALTLQTLQALYN 240
Qy 241 LAGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTLIGTQVLPSPVGNLNNMRA 300
Db 241 LAGNMDYLLTKLGVGNQLSLIGSLITGNPILYDSQTLIGTQVLPSPVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVVQVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVVQVGVSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Qy 421 RQSCNVLSLDGTLRLSGEFDATYQKNISIDQSVIVTGNLDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGTLRLSGEFDATYQKNISIDQSVIVTGNLDISTELGNVNNISNALDK 480
Qy 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVSLVCGILSLVLACILMYKQKQAKQKTLMLG 540
Db 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVSLVCGILSLVLACILMYKQKQAKQKTLMLG 540
Qy 541 NNTLDQMRATTKM 553
Db 541 NNTLDQMRATTKM 553

RESULT 14

B36830

cell fusion glycoprotein precursor - Newcastle disease virus (strain ITA/45)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: B36830
R;Toyoda, T.; Sakaguchi, T.; Hirota, H.; Gotoh, B.; Kuma, K.; Miyata, T.; Nagai, Y.
Virology 169, 273-282, 1989
A;Title: Newcastle disease virus evolution. II. Lack of gene recombination in generating
A;Reference number: A46329; MUID:89204898; PMID:2705298
A;Accession: B36830
A;Molecule type: genomic RNA
A;Residues: 1-553 <TOY>
A;Cross-references: GB:M24703
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F1-25/Domain: signal sequence #status predicted <SIG>
F126-117/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F118-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F495-528/Domain: transmembrane #status predicted <TMN>
F;85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.0%; Score 2592; DB 1; Length 553;
Best Local Similarity 94.2%; Pred. No. 2.5e-154;
Matches 521; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY	1	MSRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS	60
DB	1	MSRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS	60
QY	61	IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
DB	61	IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
QY	121	IIGGALGVATAAQTAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAVG	180
DB	121	IIGGALGVATAAQTAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAVG	180
QY	181	KMQQFVNDQFNKTAQELDCIKITQQGVNELNLYLTETTVFGPQITSPALTIQALYN	240
DB	181	KMQQFVNDQFNKTAQELDCIKITQQGVNELNLYLTETTVFGPQITSPALTIQALYN	240
QY	241	LGGNNMDYLLTKLGVGNNSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
DB	241	LGGNNMDYLLTKLGVGNNSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
QY	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLDLYCTRIVTFPMSPGIY	360
DB	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLDLYCTRIVTFPMSPGIY	360
QY	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
DB	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
QY	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
DB	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
QY	481	LEESNKLDKVNNKLTSTTSALITYLVLTVISVCCGILSVACILMYKOKAOKTLLMWG	540
DB	481	LEESNKLDKVNNKLTSTTSALITYLVLTVISVCCGILSVACILMYKOKAOKTLLMWG	540
QY	541	NTTLDQMRATTQK 553	
DB	541	NTTLDQMRATTQK 553	

RESULT 15

VGNZGB

cell fusion glycoprotein precursor - Newcastle disease virus (strain Texas G.B.)

N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: Newcastle disease virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 25-Oct-1996
C;Accession: B29201
R;Schaper, U.M.; Fuller, F.J.; Ward, M.D.W.; Mehrotra, Y.; Stone, H.O.; Stripp, B.R.;
Virology 165, 291-295, 1988
A;Title: Nucleotide sequence of the envelope protein genes of a highly virulent, neuro-
A;Reference number: A94379; MUID:88265873; PMID:3388773
A;Accession: B29201
A;Molecule type: mRNA
A;Residues: 1-553 <SCH>
A;Experimental source: strain Texas G.B.
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F1-31/Domain: signal sequence #status predicted <SIG>
F32-111/Product: cell fusion glycoprotein F2 #status predicted <FP2>
F112-116/Region: cleavage processing #status predicted
F;117-553/Product: cell fusion glycoprotein F1 #status predicted <FP1>
F;9,85,191,366,447,471/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.9%; Score 2589; DB 1; Length 553;
Best Local Similarity 92.9%; Pred. No. 3.9e-154;
Matches 514; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY	1	MSRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS	60
DB	1	MSRSSTRIPVPLMLTVRVALLSCVCPSTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS	60
QY	61	IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
DB	61	IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKGQRLIGA	120
QY	121	IIGGALGVATAAQTAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAVG	180
DB	121	IIGGALGVATAAQTAAASALIQANQANANILRLKERIAATNEAVHEVTDGLSOLAVAVG	180
QY	181	KMQQFVNDQFNKTAQELDCIKITQQGVNELNLYLTETTVFGPQITSPALTIQALYN	240
DB	181	KMQQFVNDQFNKTAQELDCIKITQQGVNELNLYLTETTVFGPQITSPALTIQALYN	240
QY	241	LGGNNMDYLLTKLGVGNNSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
DB	241	LGGNNMDYLLTKLGVGNNSLIGSLITGNPILYDSQTLLGIQVTLPSVGNLNNMRA	300
QY	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLDLYCTRIVTFPMSPGIY	360
DB	301	TYLETLSVSTTKGFASALVPKVMKGVSVIEBLDTSYCIETDLDLYCTRIVTFPMSPGIY	360
QY	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
DB	361	SCLSGNTSACMSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNGEAVSLID	420
QY	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
DB	421	RQSCNVSLDGTITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK	480
QY	481	LEESNKLDKVNNKLTSTTSALITYLVLTVISVCCGILSVACILMYKOKAOKTLLMWG	540
DB	481	LEESNKLDKVNNKLTSTTSALITYLVLTVISVCCGILSVACILMYKOKAOKTLLMWG	540
QY	541	NTTLDQMRATTQK 553	
DB	541	NTTLDQMRATTQK 553	

Search completed: April 18, 2004, 02:33:33
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 17, 2004, 06:54:07 ; Search time 97 Seconds
(without alignments)
1610.812 Million cell updates/sec

Title: US-10-725-841-2

Perfect score: 2757
Sequence: 1 MGRSSTRIPVPLMLTVRVA.....XTLLWLGNTLDQMRATTKM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2724	98.8	553	2	AAR10065
2	2716	98.5	553	6	ABR56236
3	2620	95.0	1103	6	ABR39678
4	2616	94.9	553	3	AAV51231
5	2610	94.7	553	2	AAR58858
6	2610	94.7	553	2	AAR49141
7	2610	94.7	553	2	AAW06828
8	2610	94.7	553	2	AAW10691
9	2610	94.7	553	2	AAV21983
10	2610	94.7	553	3	AAV58183
11	2610	94.7	553	3	ABR36039
12	2606	94.5	553	2	AAR14480
13	2606	94.5	553	2	AAW44941
14	2603	94.4	553	1	AAV70176
15	2493.5	90.4	564	5	ABG31709
16	2401	87.1	526	1	AAV80986
17	2386	86.5	526	2	AAV20501
18	2086.5	75.7	436	6	ABO10250
19	2065	74.9	437	4	AAU14030
20	717	26.0	529	6	ABJ18515
21	715	25.9	529	6	ABJ18516
22	714	25.9	551	6	ABJ18506
23	712	25.8	551	6	ABJ18514
24	707	25.6	551	6	ABJ18513
25	706	25.6	529	4	ABP98712

26	696.5	25.3	532	6	ABJ18507
27	694.5	25.2	538	4	ABR67476
28	689	25.0	542	2	AAR24076
29	623.5	22.6	662	2	AAR83304
30	623.5	22.6	662	5	AAW47653
31	621.5	22.5	662	3	ABR08102
32	621.5	22.5	662	4	AAW50124
33	610.5	22.1	550	2	AAR42394
34	610.5	22.1	550	4	AAR73722
35	608.5	22.1	550	2	AAR34540
36	606.5	22.0	550	2	AAR42396
37	606.5	22.0	550	2	AAR42397
38	606.5	22.0	550	2	AAR42395
39	605.5	22.0	550	2	AAW94759
40	605.5	22.0	550	4	AAR73721
41	602.5	21.9	550	2	AAW94760
42	590.5	21.4	449	6	ABJ18509
43	552	20.0	539	2	AAR39283
44	534	19.4	438	6	ABO10249
45	522.5	19.0	439	4	AAU14029

ALIGNMENTS

RESULT 1
AAR10065
ID AAR10065 standard; protein; 553 AA.
XX
AC AAR10065;
XX
DT 25-MAR-2003 (revised)
DT 14-MAR-1991 (first entry)
XX
DE Newcastle disease virus (NDV) F gene product.
XX
KW Avipoxvirus; fowlpoxvirus; vaccine.
XX
OS Newcastle disease virus.
XX
PN EP404576-A.
XX
PD 27-DEC-1990.
XX
PF 21-JUN-1990; 90EP-00306806.
XX
PR 22-JUN-1989; 89JP-00160157.
XX
PA (JAPG) NIPPON ZEON KK.
PA (SHIO) SHIONOGI & CO LTD.
XX (YANA/) YANAGIDA N.
XX Yangida N, Saeki S, Okawa S, Knamogawa K, Iritani Y, Sawaguchi K;
XX WPI: 1991-001591/01.
XX N-PSDB; AAQ10060.
XX
PT Recombinant avipox virus - contg. CDNA coding for Newcastle disease virus in region non-essential for proliferation, used as live vaccine in fowls.
XX
PS Claim 3; Fig 3; 23pp; English.
XX
CC The sequence encoding the protein may be incorporated into a recombinant CC Avipoxvirus and used as a live vaccine in fowls, providing immunity to CC fowlpoxvirus and NDV. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 553 AA;
XX

Query Match 98.8%; Score 2724; DB 2; Length 553;
Best Local Similarity 98.4%; Pred. No. 9.8e-226;
Matches 544; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALSCVCTSSLDGRPLAAAGIVTGDVAVNIYTSQTGS 60

Db 1 MGRSSTRIPVPLMLTVRMLALSCVPTSSLDGRPLAAAGIVVTDKAVNIYTSQTGS 60
 QY 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTPLDGSIIRRIQESVTTSGGKQGRLLGA 120
 Db 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTPLDGSIIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
 Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETLVFGPQITSPALTOITQALYN 240
 Db 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETLVFGPQITSPALTOITQALYN 240
 QY 241 LAGGNMDYLLTKLGVGNNSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 Db 241 LAGGNMDYLLTKLGVGNNSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
 QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 Db 301 TYLETLSVSTTKGFASALVPKVMKVGSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360
 QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNTGEAVSLID 420
 Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNTGEAVSLID 420
 QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
 Db 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480
 QY 481 LEESNSKLDKVNKLTSTSTALITYIVTLVISLVCGLSLVLACLYMYKQKQKTLMLWG 540
 Db 481 LEESNSKLDKVNKLTSTSTALITYIVTLVISLVCGLSLVLACLYMYKQKQKTLMLWG 540
 QY 541 NNTLDQMRATTKM 553
 Db 541 NNTLDQMRATTKM 553

RESULT 2

ABR36236
 ID ABR56236 standard; protein; 553 AA.

XX AC ABR56236;

XX DT 20-NOV-2003 (first entry)

XX DE Newcastle disease virus (NDV) Fusion (F)-protein.

XX KW F-protein; virucide; vaccine; anti-viral; Fusion protein;
 protein co-ordinate data.

XX OS Newcastle disease virus.

XX FN WO2003040178-A1.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-AU001522.

XX PR 09-NOV-2001; 2001AU-00008784.

XX PA (BIOT-) BIOTA HOLDINGS LTD.

XX PI Morton CJ, Parker MW, Ryan J;

XX DR WPI; 2003-441524/41.

XX PT Identifying, screening or modifying anti-viral agents, by generating a 3-
 dimensional structure model of respiratory syncytial virus-F protein
 having a target site to interact with an anti-viral agent that inhibit
 RSV-F.

XX PS

XX CC Disclosure; Fig 1; 224pp; English.

XX CC The present invention relates to a method (M1) for identifying a
 candidate anti-viral agent (I), screening compounds and/or chemical
 complexes for (I), modifying (I) to improve anti-viral activity, or
 producing anti-viral agents, by generating a 3-dimensional structure
 model of Respiratory Syncytial Virus (RSV) Fusion (F)-protein with 3-
 dimensional structure of target site to which an anti-viral agent may
 interact and thus inhibit RSV-F protein activity. The present sequence is
 the Newcastle Disease Virus (NDV) F-protein used in a sequence alignment
 with the RSV F-protein sequence (ABR56234)

XX SQ Sequence 553 AA;

Query Match 98.5%; Score 2716; DB 6; Length 553;

Best Local Similarity 98.2%; Pred. No. 4.8e-225;

Matches 543; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTDKAVNIYTSQTGS 60

Db 1 MGRSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTDKAVNIYTSQTGS 60

QY 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTPLDGSIIRRIQESVTTSGGKQGRLLGA 120

Db 61 IIVKLLPNMPKDKKACAPLEAYNRTLTLLTPLDGSIIRRIQESVTTSGGKQGRLLGA 120

QY 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180

Db 121 IIGGAALGVATAAQITAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180

QY 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETLVFGPQITSPALTOITQALYN 240

Db 181 KMQQFVNDQFNKTAQELDCIKITQGVGVELNLYLTETLVFGPQITSPALTOITQALYN 240

QY 241 LAGGNMDYLLTKLGVGNNSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

Db 241 LAGGNMDYLLTKLGVGNNSLIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

QY 301 TYLETLSVSTTKGFASALVPKVMKVGSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360

Db 301 TYLETLSVSTTKGFASALVPKVMKVGSVIEBELDTSYCIETDLDLYCTRIVTFPMSPGIY 360

QY 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNTGEAVSLID 420

Db 361 SCLSGNTSACMSYKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNTGEAVSLID 420

QY 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480

Db 421 ROSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLDISTELGNVNNISNALDK 480

QY 481 LEESNSKLDKVNKLTSTSTALITYIVTLVISLVCGLSLVLACLYMYKQKQKTLMLWG 540

Db 481 LEESNSKLDKVNKLTSTSTALITYIVTLVISLVCGLSLVLACLYMYKQKQKTLMLWG 540

QY 541 NNTLDQMRATTKM 553

Db 541 NNTLDQMRATTKM 553

RESULT 3

ABR39678

ID ABR39678 standard; protein; 1103 AA.

XX AC ABR39678;

XX DT 23-JUN-2003 (first entry)

XX DE Amino acid sequence of F protein and partial HN protein.

XX KW NDV; lentogenic; oncolytic; fusion glycoprotein; F gene; HN gene;
 haemagglutinin-neuraminidase; cytostatic; gene therapy; cancer.

25-MAR-2003 (revised)
14-APR-1995 (first entry)
Newcastle disease virus F gene product.
Newcastle disease virus; F gene; SfiI; vector 502-26.22.
Synthetic.
W09419015-A1.
01-SEP-1994.
28-FEB-1994; 94WO-US002252.
26-FEB-1993; 93US-00024156.
(SYTR) SYNTRO CORP.
Cochran MD;
WPI; 1994-294008/36.
N-PSDB; AAQ70570.
New recombinant fowl pox viruses - useful as vaccines against fowl pox virus, Newcastle Disease Virus and infectious laryngotracheitis virus.
Disclosure; Page 79-81; 97pp; English.
AAQ70570 is the SfiI fragment insert in Homology Vector 502-26.22 contg. Newcastle disease virus (NDV) HN and F genes. The structure of the fragment is: 5'- Junction A - Fragment 1 (NDV HN AAs 2-577) - Junction B - Fragment 2 (NDV F AAs 1-553) - Junction C - Fragment 3 (pBR322) - Junction D - 3'. Fragment 1 is Avail to NaeI fragment of the full length NDV HN cDNA clone (BJ strain). Fragment 2 is BamHI to PstI fragment of the full length NDV F cDNA (B1 strain). Fragment 3 is a PstI and Scal fragment of pBR322. The structures of the junctions A, B, C and D are given in AAQ70552, AAQ70553, AAQ70554 and AAQ70555 respectively. (Updated on 25-MAR-2003 to correct PN field.)
Sequence 553 AA;
Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGSRSSTIPVPLMLTVRVVALALSCVPTSSLDGRLAAGIVTGDKAIVNLYTSQTGS 60
DB 1 MGSRETKNPAPMLTIRVALVLSCTPANSIDGRLAAGIVTGDKAIVNLYTSQTGS 60
QY 61 ITVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 ITVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 ITGGALGVATAAQITAAASALIQANONANILRLKERIAATNEAVHEVTDGSLAVAVG 180
DB 121 ITGGALGVATAAQITAAALIAQAKQANANILRLKESIAATNEAVHEVTDGSLAVAVG 180
QY 181 KMQQFVNDQFNKTAQELDCIKIQQGVVELNLYLTLLTFVGPQITSPALTIQALYN 240
DB 181 KMQQFVNDQFNKTAQELDCIKIAQQGVVELNLYLTSTTVFGQIISPALNKLTIQALYN 240
QY 241 LAGGNMDYLLTKLGVGNQNLSSLIGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
DB 241 LAGGNMDYLLTKLIGNNQNLSSLIGSLITGNPILYDSQTLGLIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTTPMSPGIY 360
DB 301 TYLETLSVSTTRGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIVTTPMSPGIY 360
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPLIISQNYGEAVSLID 420

QY 421 RQCNVLSDGITLRLSGEDFATYQKNISIQDSQVITGNLDISTELGNVNNISNALDK 480
DB 421 KQCNVLSDGITLRLSGEDFATYQKNISIQDSQVITGNLDISTELGNVNNISNALNK 480
QY 481 LEESNKLDKVNVKLTSTSAIIVITVLSVCGILSLVLAACYLKYKAKAQKTLMLG 540
DB 481 LEESNKLDKVNVKLTSTSAIIVITVLSVCGILSLVLAACYLKYKAKAQKTLMLG 540
QY 541 NNTLDDQMRATTCKM 553
DB 541 NNTLDDQMRATTCKM 553
RESULT 7
AAW06828
ID AAW06828 standard; protein; 553 AA.
XX AC AAW06828;
XX DT 04-MAR-1997 (first entry)
XX DE Newcastle disease virus F gene product.
XX KW Turkey herpes Virus; recombinant virus; vaccine; prophylaxis;
KW immunisation; avian virus; infectious bronchitis virus;
KW infectious bursal disease virus; Newcastle disease virus;
KW Marek's disease virus; infectious laryngotracheitis virus; IBV; IBDV;
KW NDV; MDV; ILV.
XX OS Newcastle disease virus.
XX PN W09605291-A1.
XX PD 22-FEB-1996.
XX PF 09-AUG-1995; 95WO-US010245.
XX PR 09-AUG-1994; 94US-00288065.
XX PR 22-DEC-1994; 94US-00362240.
XX PA (SYTR) SYNTRO CORP.
XX PI Cochran MD, Junker DE, Wild MA, Singer PA;
XX DR WPI; 1996-139689/14.
XX PT N-PSDB; AAT18203.
XX PT Recombinant turkey herpes viruses contg. foreign DNA encoding a cytokine
XX - useful in vaccines to protect against Marek's disease virus and other
XX avian viruses.
XX PS Disclosure; Page 179-180; 249pp; English.
XX CC Recombinant turkey herpes virus (rTH) which comprise a foreign DNA
XX sequence encoding a cytokine inserted into a XhoI site within an EcoRI #9
XX genomic fragment, where the cytokine can be expressed in host cells
XX infected with the virus can be used in vaccines to protect turkeys
XX against avian viruses. The recombinant viruses can be used for immunising
XX birds against infectious bronchitis virus (IBV), infectious bursal
XX disease virus (IBDV), Marek's disease virus (MDV), infectious
XX laryngotracheitis virus (ILV) and Newcastle disease virus (NDV). They may
XX also be used in multivalent vaccines to protect against two or more of
XX these avian viruses. This sequence is the product of the F gene of the
XX Newcastle disease virus and is an antigen which can be used in the
XX recombinant vaccines
SQ Sequence 553 AA;
Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;


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PN US925358-A.
XX 20-JUL-1999.
XX 07-JUN-1995; 95US-00484575.
XX 26-FEB-1993; 91US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX (SYTR ) SYNTRO CORP.
XX Junker DE, Cochran MD;
XX WPI: 1999-418249/35.
XX N-PSDB; AAX81147.
XX Fowlpox viruses, useful as vaccines for immunization of chickens/turkeys
XX against Fowlpox and Newcastle disease virus.
XX Disclosure; Col 61-70; 108pp; English.
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a region of the fowlpox virus genome
XX corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a
XX host cell. The virus is used as a vaccine for immunising chickens against
XX Newcastle disease virus (NDV), Fowlpox, and infectious Laryngotracheitis
XX Sequence 553 AA;
SQ
Query Match 94.7%; Score 2610; DB 2; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
DB 1 MGRSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
QY 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTFLGDSIRRIQESVTTSGGKQGRLLGA 120
DB 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTFLGDSIRRIQESVTTSGGKQGRLLGA 120
QY 121 IIGGVALGVATAAQITAAALIQAKQNAANILFLKESIAATNEAVHEVTDGLSOLAVAVG 180
DB 121 IIGGVALGVATAAQITAAALIQAKQNAANILFLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKIAQQVGVNELNLTETTVFGPQITSPALTIQALYN 240
DB 181 KMOQFVNDQFNKTAQELDCIKIAQQVGVNELNLTETTVFGPQITSPALTIQALYN 240
QY 241 LAGGNDYLLTKLGVGNQSLIGSLITGNFILDYDSOTQLLGIQVTLPSVGNLNMRA 300
DB 241 LAGGNDYLLTKLGVGNQSLIGSLITGNFILDYDSOTQLLGIQVTLPSVGNLNMRA 300
QY 301 TYLETLVSVTTGTFASALVPKVKVGVIEELDTSCYIETDLDLYCTRTVTFPMSPGIY 360
DB 301 TYLETLVSVTTGTFASALVPKVKVGVIEELDTSCYIETDLDLYCTRTVTFPMSPGIY 360
QY 361 SCLSGNTSACWYKTEGALTPMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 361 SCLSGNTSACWYKTEGALTPMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
QY 421 QKCNVLSLGGITLRLSGEFDTATYQKNISIQDSQVITGNLIDISTELGNVNSISNALDK 480
DB 421 QKCNVLSLGGITLRLSGEFDTATYQKNISIQDSQVITGNLIDISTELGNVNSISNALDK 480
QY 481 LEESSKLDKVNKLTSTSLIITVIVTLVTSVCGILSVLACVIMYKQAKQKTLILWG 540
DB 481 LEESSKLDKVNKLTSTSLIITVIVTLVTSVCGILSVLACVIMYKQAKQKTLILWG 540
QY 541 NNTLDQWRATTKM 553
DB 541 NNTLDQWRATTKM 553
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RESULT 10

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AA58183
ID AAY58183 standard; protein; 553 AA.
XX AAY58183;
XX 14-MAR-2000 (first entry)
XX NDV fusion (F) protein.
XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;
XX infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
XX Marek's disease virus; cytokerin; promoter; homologous recombination;
XX homology vector; multivalent; live vaccine; fusion protein.
XX Newcastle disease virus.
XX Key Location/Qualifiers
XX Domain 501..527
XX /note= "Transmembrane anchor domain"
XX US6001369-A.
XX 14-DEC-1999.
XX 07-JUN-1995; 95US-00477459.
XX 26-FEB-1993; 93US-00024156.
XX 28-FEB-1994; 94WO-US002252.
XX (SYTR ) SYNTRO CORP.
XX Junker DE, Cochran MD;
XX WPI: 2000-071638/06.
XX N-PSDB; AAX49295.
XX Recombinant fowlpox virus useful as a vaccine for immunizing fowl against
XX Marek's disease, Newcastle disease, Infectious Laryngotracheitis Virus
XX and/or fowlpox.
XX Claim 5; Col 71-74; 56pp; English.
XX The invention relates to a recombinant fowlpox virus (FPV) comprising a
XX foreign DNA inserted into a 4.2 kb EcoRI fragment of the fowlpox virus
XX genome. The foreign DNA is capable of being expressed in a host cell into
XX which the fowlpox virus has been introduced and encodes an antigenic
XX protein. The antigenic protein which may be expressed includes infectious
XX laryngotracheitis virus (ILTV) glycoprotein B (gB) or glycoprotein D (gD),
XX AAY58184, Newcastle disease virus (NDV) haemagglutinin (HN, AAY58182) or
XX fusion (F) protein (AAY58183) and Marek's disease virus gB or gD. The
XX foreign DNA may alternatively encode a cytokine such as chicken
XX myelomonocytic growth factor (CMGF) or chicken interferon (cIFN). The
XX foreign DNA in the recombinant FPV is under the control of one or more
XX synthetic pox promoters, enabling control of strength and timing of
XX heterologous gene expression. The synthetic pox virus promoters that may
XX be used are based on promoters of the vaccinia virus and include early
XX promoter 1 (EPI), late promoter 1 (LPI), EP2 and LP2 (AAZ49291-249294,
XX respectively). The recombinant FPV is generated via homologous
XX recombination between FPV DNA and a homology vector containing the
XX foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
XX the invention are used as multivalent live vaccines for immunising fowl
XX against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
XX present sequence represents NDV fusion (F) protein
XX Sequence 553 AA;
SQ
Query Match 94.7%; Score 2610; DB 3; Length 553;
Best Local Similarity 93.1%; Pred. No. 6.7e-216;
Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;
QY 1 MGRSTRIPVPLMLTVRVALSCVPTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
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Db 1 MGRSPSTKPNPAPMLTIRVALVLSICPANSIDGRPLAAGIVVTGDKAVNIYTSSTGTS 60
Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120
Qy 121 IIGGAALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGVALGVATAAQITTAASALIQANONANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240
Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTETLTVFGPQITSPALNKLTIOALYN 240
Qy 241 LAGGNMDYLLTKLGVNNQLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Db 241 LAGGNMDYLLTKLIGINNQLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300
Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMTRVGSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360
Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420
Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISONYGEAVSLID 420
Qy 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNALDK 480
Db 421 KQSCNVLSIGGITLRLSGEFVDTYQKNISIODSQVITGNLDISTELGNVNNISNALNK 480
Qy 481 LEESNKLKDVNKLSTSTALITYIVLTIVISVCGILSVLACLYMKAKOQKTLMLWG 540
Db 481 LEESNRKLDKVNKLSTSTALITYIVLTIVISVCGILSVLACLYMKAKOQKTLMLWG 540
Qy 541 NNTLDQMRATTM 553
Db 541 NNTLDQMRATTM 553
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RESULT 11

AAB36039
ID AAB36039 standard; protein; 553 AA.

XX AAB36039;

XX 06-AUG-2003 (revised)

DT 02-MAR-2001 (first entry)

DE Protein encoded by NDV SfiI fragment.

KW Fowlpox virus; FPV; antiviral; antibacterial; vaccine;

KW Newcastle's disease virus; NDV; Marek's disease;

KW infectious laryngotracheitis.

XX Newcastle disease virus.

XX US6136318-A.

XX 24-OCT-2000.

XX 07-JUN-1995; 95US-00486414.

XX 26-FEB-1993; 93US-00024156.

PR 28-FEB-1994; 94WO-US002252.

XX (JUNK/) JUNKER D E.

PA (COCH/) COCHRAN M D.

XX Cochran MD, Junker DE;

XX WPI: 2000-686071/67.

XX N-PSDB; AAC67862.

XX New recombinant fowlpox virus useful as vaccines contains foreign DNA
PT inserted into specific non-essential region of the genome.
XX Disclosure; Col 71-74; 56pp; English.

XX The present sequence is provided in a specification relating to a
CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted
CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA
CC can be expressed in host cells infected with FPV. The recombinant FPV may
CC be used in vaccines to protect animals (especially chickens) against
CC fowlpox and, depending on the source of the foreign DNA, other diseases,
CC particularly Newcastle's disease, Marek's disease or infectious
CC laryngotracheitis. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 553 AA;

Query Match 94.7%; Score 2610; DB 3; Length 553;

Best Local Similarity 93.1%; Pred. NO. 6.7e-216;

Matches 515; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGRSSTRIPVPLMLTIRVALVLSICPANSIDGRPLAAGIVVTGDKAVNIYTSSTGTS 60

Db 1 MGRSSTRIPVPLMLTIRVALVLSICPANSIDGRPLAAGIVVTGDKAVNIYTSSTGTS 60

Qy 61 IIVKLLPNPKDKEACAKAPLEAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

Db 61 IIVKLLPNLPKDEACAKAPLDAYNRTLTLLTPLGDSIRRIQESVTTSGGKQGRLLGA 120

Qy 121 IIGGAALGVATAAQITTAASALIQANONANILRLKRIIAATNEAVHEVTDGLSOLAVAVG 180

Db 121 IIGVALGVATAAQITTAASALIQANONANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180

Qy 181 KMQQFVNDQFNKTAQELDCIKITQQVGVNELNLYLTETLTVFGPQITSPALTIQALYN 240

Db 181 KMQQFVNDQFNKTAQELDCIKIAQQVGVNELNLYLTETLTVFGPQITSPALNKLTIOALYN 240

Qy 241 LAGGNMDYLLTKLGVNNQLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

Db 241 LAGGNMDYLLTKLIGINNQLSSLIIGSLITGNPILYDSOTQLLGIQVTLPSVGNLNNMRA 300

Qy 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360

Db 301 TYLETLSVSTTKGFASALVPKVMTRVGSVIEELDTSYCIETDLDLYCTRIIVTFPMSPGIY 360

Qy 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISONYGEAVSLID 420

Db 361 SCLSGNTSACMYSKTEGALTTPYMTIKGSVIANCKMTTCRCVNPFGIISONYGEAVSLID 420

Qy 421 ROSCNVLSIDGITLRLSGEFDATYQKNISIODSQVITGNLDISTELGNVNNISNALDK 480

Db 421 KQSCNVLSIGGITLRLSGEFVDTYQKNISIODSQVITGNLDISTELGNVNNISNALNK 480

Qy 481 LEESNKLKDVNKLSTSTALITYIVLTIVISVCGILSVLACLYMKAKOQKTLMLWG 540

Db 481 LEESNRKLDKVNKLSTSTALITYIVLTIVISVCGILSVLACLYMKAKOQKTLMLWG 540

Qy 541 NNTLDQMRATTM 553

Db 541 NNTLDQMRATTM 553

RESULT 12

AAR14480

ID AAR14480 standard; protein; 553 AA.

XX AAR14480;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 27-NOV-1991 (first entry)

XX Newcastle disease virus immunogenic fusion protein.

XX avian influenza; recombinant poultry virus vaccine; HVT;
 KW Turkey Herpes Virus.

XX Newcastle disease virus (STRAIN TEXAS).

OS EP447303-A.

XX 18-SEP-1991.

XX 07-MAR-1991; 91EP-00400634.

XX 12-MAR-1990; 90FR-00003105.

XX (INMR) RHONE MERIEUX SA.

XX Reysenelon A, Kohen G;

XX WPI; 1991-275886/38.

XX N-PSDB; AAQ13668.

XX New herpes recombinants - useful as vaccines against human and animal
 PT viral conditions, e.g. fowl:pest, coccidiosis and pasteurellosis, etc.

XX Example 3; Page 17-19; 22pp; French.

XX This sequence is an immunogenic Newcastle Disease Virus fusion protein.
 CC It can be inserted into the RR2 (ribonucleotide reductase small subunit)
 CC gene of the Turkey Herpes Virus. The HVT is suitable for use in live
 CC vaccines as it is apathogenic and non-oncogenic. Other vaccines are
 CC constructed in a similar way using immunogens which protect against e.g.
 CC avian infectious bronchitis, colibacillosis, Marek Disease, Gumboro
 CC Disease, avian anaemia, etc. See also AAQ13430. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 553 AA;

Query Match 94.5%; Score 2606; DB 2; Length 553;
 Best Local Similarity 94.8%; Pred. No. 1.5e-215;
 Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 DB 1 MGRSSTRIPVPLMLTRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 QY 61 IIVKLLPNMPKDEKAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 DB 61 IIVKLLPNMPKDEKAKAPLEAYNRTLTLLPLGDSIRRIQESVTTSGGKQGRLLGA 120
 QY 121 IIGGAALGVATAQITTAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
 DB 121 IIGSVLGVATAQITTAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
 QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTLTFFGQITSPALTQTIOALYN 240
 DB 181 KMQQFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTLTFFGQITSPALTQTIOALYN 240
 QY 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPTLYDSQTQLLGIQVTLFSGVGNLNMRA 300
 DB 241 LAGNMDYLLTKLGVGNQNLSSLIGSLITGNPTLYDSQTQLLGIQVTLFSGVGNLNMRA 300
 QY 301 TYLETLSSVTTKGFASALNPKVVMKGVSVIEELDTSYCIETDLDLXCTRIVTTPMSPGIY 360
 DB 301 TYLETLSSVTTKGFASALNPKVVMKGVSVIEELDTSYCIETDLDLXCTRIVTTPMSPGIY 360
 QY 361 SCLSGNTSACWYSKTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 DB 361 SCLSGNTSACWYSKTEGALTPPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
 QY 421 ROSCNVLSLGDITIRLSGEFATYQKNISODSOVITGNLIDISTELGNVNNISNALDK 480
 DB 421 RHSCNVLSLGDITIRLSGEFATYQKNISILDSQVITVGNLIDISTELGNVNNISNALNK 480

QY 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVTSLVCGILSLVLAICYLMTYKQKAAQKTLWLIG 540
 DB 481 LEESNSKLDKVNKLTSTSTALITYIVLTIVTSLVCGILSLVLAICYLMTYKQKAAQKTLWLIG 540
 QY 541 NNTLDQMRATTKM 553
 DB 541 NNTLDQMRATTKI 553

RESULT 13

AAW44941

ID AAW44941 standard; protein; 553 AA.

XX AC AAW44941;

XX 28-OCT-1998 (first entry)

XX Newcastle disease virus glycoprotein F.

XX Multivalent vaccine; bird; pathogen; respiratory disease; MDV; NDV; IBDV;
 KW digestive disease; Marek's disease virus; Newcastle disease virus; CAV;
 KW infectious bursal disease virus; Gumboro disease virus; vaccine; ILTV;
 KW avian infectious bronchitis virus; IBV; chicken anaemia virus; AEV; PCR;
 KW infectious laryngotracheitis virus; avian encephalomyelitis virus; TRTV;
 KW turkey rhinotracheitis virus; influenza virus A avian; vector; primer;
 KW amplification; glycoprotein; gallid herpesvirus.

XX Newcastle disease virus.

XX FR2751225-A1.

XX 23-JAN-1998.

XX 19-JUL-1996; 96FR-00009339.

XX 19-JUL-1996; 96FR-00009339.

XX (INMR) RHONE MERIEUX SA.

XX Audomnet JCF, Bouchardon A, Riviere MEA;

XX WPI; 1998-112825/11.

XX N-PSDB; AAV49342.

XX Multi-valent polynucleotide vaccines against avian pathogens - consist of
 PT at least 3 plasmids able to express protective antigens from specified
 PT viruses.

XX Example 10; Fig 6; 55pp; French.

XX The invention relates to a multivalent vaccine for protecting birds
 CC against several pathogens, especially pathogens associated with
 CC respiratory and digestive diseases. The pathogens are especially selected
 CC from Marek's disease virus (MDV), Newcastle disease virus (NDV),
 CC infectious bursal disease virus (IBDV), avian infectious bronchitis virus
 CC (IBV), chicken anaemia virus (CAV), infectious laryngotracheitis virus
 CC (ILT), avian encephalomyelitis virus (AEV), turkey rhinotracheitis virus
 CC (TRTV) and influenza virus A avian (AIV). The vaccines are preferably
 CC composed of polynucleotide sequences encoding 3 antigens, all as part of
 CC vectors. This sequence represents the NDV strain Texas GB glycoprotein F.
 CC The coding sequence was subcloned into the plasmid pVR1012 to generate
 CC plasmid pAB047 for use in the vaccine

XX Sequence 553 AA;

Query Match 94.5%; Score 2606; DB 2; Length 553;
 Best Local Similarity 94.8%; Pred. No. 1.5e-215;
 Matches 524; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGRSSTRIPVPLMLTRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60
 DB 1 MGRSSTRIPVPLMLTRVALALSCVCPSTSSLDGRPLAAGIVTGDKAVNIYTSSQTGS 60

QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIORSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIORSVTTSGGKQGRLLGA 120
QY 121 IIGGALGVATAAQTAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGGALGVATAAQTAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPOITSPALTIQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKIAQOVGVNELNLYLTTELTVFGPOITSPALTIQALYN 240
QY 241 LAGNNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLQIGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLQIGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYICETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYICETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSAITYIVTLVTLVSVCGILSLVACVLMYKQAKQKTLWLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITYIVTLVTLVSVCGILSLVACVLMYKQAKQKTLWLWG 540
QY 541 NNTLDQMRATTCK 553
Db 541 NNTLDQMRATTCK 553

RESULT 14

AAP70176
ID AAP70176 standard; protein; 553 AA.
AC AAP70176;
XX XX
XX XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-APR-1991 (first entry)
XX XX
DE Sequence of Newcastle Disease Virus (NDV) F polypeptide.
XX Epitope; probe; diagnosis.
XX Newcastle disease virus.
XX EP227414-A.
XX 01-JUL-1987.
XX 16-DEC-1986; 86EP-00309804.
XX 18-DEC-1985; 85GB-00031147.
XX 14-APR-1986; 86GB-00009037.
XX 15-JUL-1986; 86US-00885765.
XX (NATR) NAT RES DEV CORP.
XX Bingham RW, Chambers P, Emerson PT, Millar NS;
PI WPI, 1987-179630/26.
DR N-PSDB; AAN70261.
XX Newcastle disease virus gene clones - comprise polynucleotide(s) encoding
PT the HN and/or F protein of Newcastle disease virus RNA.

XX Example; Page 11-16; 22pp; English.
XX An artificial polynucleotide encoding an HN and/or F polypeptide of
CC Newcastle Disease Virus (NDV) DNA, a bioprecursor of the polypeptide, or
CC an epitopic portion of the polypeptide or an artificial nucleotide
CC complementary to the polynucleotide are claimed. The polynucleotides are
CC useful for preparing a probe for extracting similar genes from a gene
CC library or for identifying the presence of NDV virions in a sample obd.
CC from poultry. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 27-AUG-2003 to correct OS field.)
XX Sequence 553 AA;

Query Match 94.4%; Score 2603; DB 1; Length 553;
Best Local Similarity 93.5%; Pred. No. 2.7e-215;
Matches 517; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGRSSSTRIPVPLMLTVRVALALSCVPTSSLDGRPLAAAGIVVTGKAVNIYTSQTGS 60
Db 1 MGRSPSTKPNVPMPLTVRVALVLSICPANSIDGRPLAAAGIVVTGKAVNIYTSQTGS 60
QY 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIORSVTTSGGKQGRLLGA 120
Db 61 IIVKLLPNMPKDEACAKAPLEAYNRTLTLLTPLGDSIRRIORSVTTSGGKQGRLLGA 120
QY 121 IIGGALGVATAAQTAAASALIQANQNAANILRLKERIAATNEAVHEVTDGLSOLAVAVG 180
Db 121 IIGGALGVATAAQTAAASALIQANQNAANILRLKESIAATNEAVHEVTDGLSOLAVAVG 180
QY 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPOITSPALTIQALYN 240
Db 181 KMOQFVNDQFNKTAQELDCIKITQOVGVNELNLYLTTELTVFGPOITSPALTIQALYN 240
QY 241 LAGNNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLQIGIQVTLPSVGNLNNMRA 300
Db 241 LAGNNMDYLLTKLGVGNQNLSSLGSLITGNPILYDSQTLQIGIQVTLPSVGNLNNMRA 300
QY 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYICETDLDLYCTRIVTFPMSPGIY 360
Db 301 TYLETLSVSTTKGFASALVPKVMKGVSVIEELDTSCYICETDLDLYCTRIVTFPMSPGIY 360
QY 361 SCLSGNTSACMSKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
Db 361 SCLSGNTSACMSKTEGALTTPYMLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLID 420
QY 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
Db 421 RQSCNVLSLDGITLRLSGEFDATYQKNISIQDSQVIVTGNLIDISTELGNVNNISNALDK 480
QY 481 LEESNSKLDKVNKLTSTSAITYIVTLVTLVSVCGILSLVACVLMYKQAKQKTLWLWG 540
Db 481 LEESNSKLDKVNKLTSTSAITYIVTLVTLVSVCGILSLVACVLMYKQAKQKTLWLWG 540
QY 541 NNTLDQMRATTCK 553
Db 541 NNTLDQMRATTCK 553

RESULT 15

ABG31709
ID ABG31709 standard; protein; 564 AA.
XX ABG31709;
AC ABG31709;
XX 15-NOV-2002 (first entry)
DT Newcastle disease virus (NDV) fusion protein.

DE Newcastle disease virus; NDV; novel recombinant avian herpesvirus; NAHV;
KW herpes virus of turkeys; HVT; Marek's disease; Newcastle disease;
XX infectious laryngotracheitis; virucide; immunostimulant; vaccine.
XX

OS Newcastle disease virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 54 /label= unknown
FT /note= "Encoded by CTN"
XX
PN US2002081316-A1.
XX
XX PD 27-JUN-2002.
XX
XX PF 14-JUN-2001; 2001US-00881457.
XX
PR 12-JUN-1992; 92US-00898087.
PR 26-FEB-1993; 93US-00023610.
PR 14-JUN-1993; 93WO-US005681.
PR 09-AUG-1994; 94US-00288065.
PR 09-AUG-1995; 95WO-US010245.
PR 13-JUN-1996; 96US-00663566.
PR 21-FEB-1997; 97US-00804372.
PR 25-OCT-1999; 99US-00426352.
XX
PA (COCH/) COCHRAN M D.
PA (COOK/) COOK S M.
PA (WILD/) WILD M A.
XX
PI Cochran MD, Cook SM, Wild MA;
XX
XX WPI; 2002-635456/68.
XX N-PSDB; ABK90556.
XX
PT Novel recombinant avian herpesvirus comprising unique long and repeat
PT viral genome regions of herpes virus of turkeys, unique short viral
PT genome region of Marek's disease virus, and optional foreign DNA
PT sequence.
XX
XX Disclosure; Page 14-16; 26pp; English.
XX
XX The invention relates to a novel recombinant avian herpesvirus (NAHV)
CC comprising a herpes virus of turkeys (HVT) unique long (UL) and repeat
CC viral genome region and a Marek's disease virus unique short (US) viral
CC genome region where at least one foreign DNA sequence is inserted within
CC a US2 gene of the US region of the NAHV, and is capable of being
CC expressed in a host cell. NAHV is useful for producing vaccines used for
CC immunising an avian species against Newcastle disease, infectious
CC laryngotracheitis and Marek's disease. This sequence represents a
CC Newcastle disease virus (NDV) fusion protein
XX
XX Sequence 564 AA;

Search completed: April 18, 2004, 01:23:38
Job time : 103 secs

Query Match 90.4%; Score 2493.5; DB 5; Length 564;
Best Local Similarity 89.7%; Pred. No. 7.8e-206;
Matches 496; Conservative 24; Mismatches 32; Indels 1; Gaps 1;
QY 1 MGSRSSTRIPLVPLMIVRVALALSCVCTSSLDGRPLAAGIVVTGDKAVNIYTSQTGS 60
DB 13 MGSRPSTKPPAPMMLTTRVALVLSICIPANSIDGRPLAAGXWLOETKQ-STYTPHPROV 71
QY 61 IIVKLLNMPKDKACAKAPLEAYNRTLLTLPGLDSIRRIQBSVTTSGGKQGRLLGA 120
DB 72 NHIKLLNPLPKDKACAKAPLDAYNRTLLTLPGLDSIRRIQBSVTTSGGKQGRLLGA 131
QY 121 IIGGAALGVATAAQITAAALIQANQNAANILRLKERIAATNEAVHEVTDGLSQLAVAG 180
DB 132 IIGGVALGVATAAQITAAALIQANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAG 191
QY 181 KMQQFVNDQFNKTAQELDCIKITQOVGVFELNLYLTETTFVGPQITSPALQTOLTIQALYN 240
DB 192 KMQQFVNDQFNKTAQELDCIKIAQOVGVFELNLYLTETTFVGPQITSPALNKLTIOALYN 251
QY 241 LAGGNMYYLLTKLGVGNQSLSSIGSLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA 300
DB 252 LAGGNMYYLLTKLIGGNQSLSSIGSLITGNPILYDSOTQLIGIQVTLPSVGNLNNMRA 311

QY 301 TYLETILSVSTTKGFASALVPKVMKVGSVIEELDTSYCIETDLDLCTRIVTTPMSPGIY 360
DB 312 TYLETILSVSTTRGFASALVPKVVTRVGSVIEELDTSYCIETDLDLCTRIVTTPMSPGIY 371
QY 361 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIIISQNYGEAVSLID 420
DB 372 SCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCVNPPIIISQNYGEAVSLID 431
QY 421 ROSCNVLSLDGITRLSGEPDATYQKNISIQDSQVITVGNLDISTELGNVNNISNALDK 480
DB 432 KQSCNVLSLGGITRLSGEPDVYQKNISIQDSQVITVGNLDISTELGNVNNISNALNK 491
QY 481 LEESNSKLDKVNKLTSTSAITYIVLTIVISVCGLSLVACVLMYKOKAQOKTLLWLIG 540
DB 492 LEESNEKLDKVNKLTSTSAITYIVLTIVISVCGLSLVACVLMYKOKAQOKTLLWLIG 551
QY 541 NNTLDQMRATTKM 553
DB 552 NNTLDQMRATTKM 564

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